

FIG. 1A

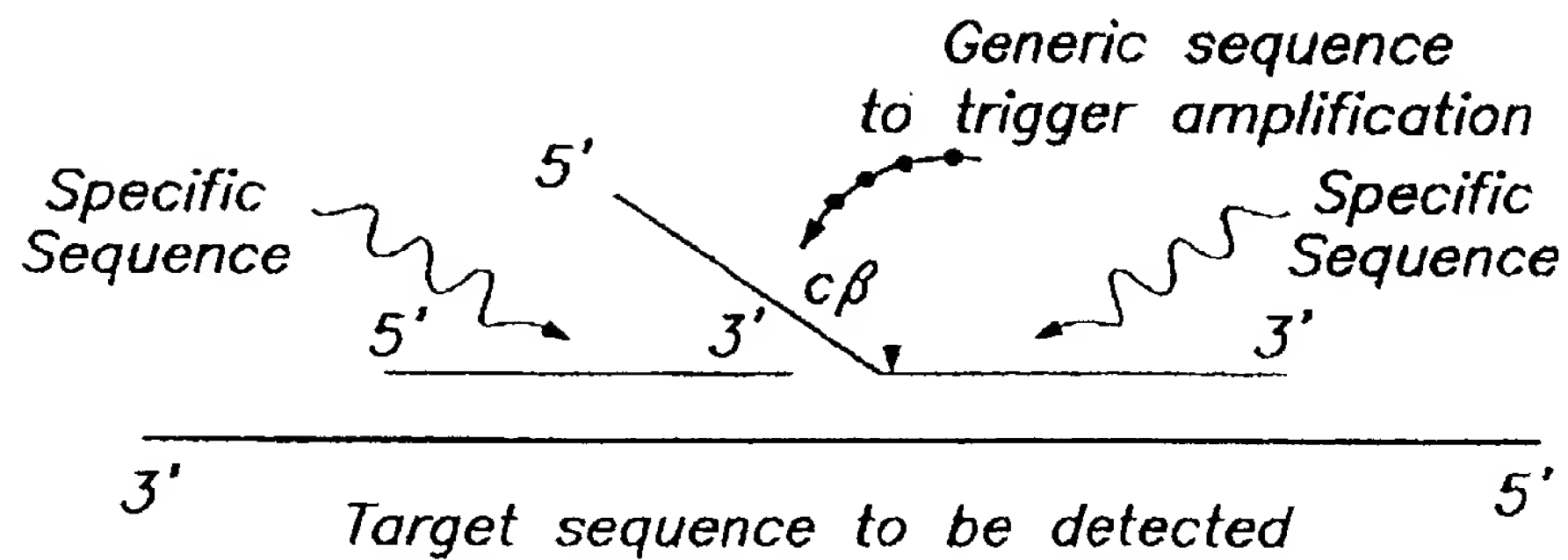


FIG. 1B PART ONE: TRIGGER REACTION

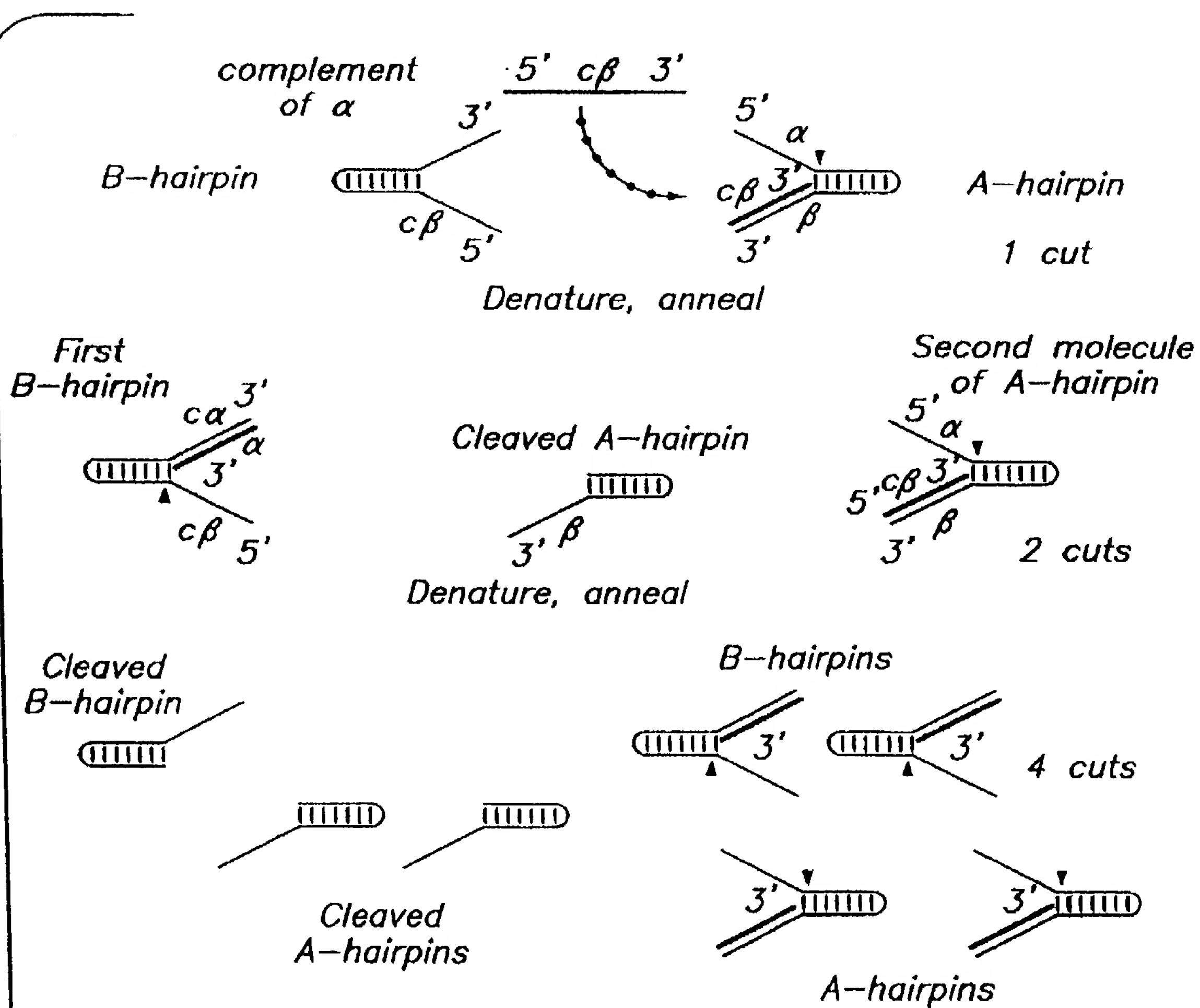


FIG. 1C PART TWO: DETECTION REACTION

.	A								G	347
.	G	T	A . C	T	G . G	T	T	I		344
.	T . A . C		350

FIG. 2B

MAJORITY [SEQ ID NO:7] CGAGGCGGAGGAGGTGTGGCCACCTGGCCAGAAAGGCGGAAAGGAGGGTACGAGGTGGGCATCCTC

DNAPTAQ [SEQ ID NO:1]C.....G.....C.....C..... 417
 DNAPTFL [SEQ ID NO:2] T.....G.....CG..... 414
 DNAPTTH [SEQ ID NO:3]T..C..... 420

MAJORITY ACCGCGGAGCGGAGCTCTACGAGCTCTTCCGACCGCATGGCGTCTCCACCCGAGGGGTACCTCA

DNAPTAQAAA.....T.....CA..... 487
 DNAPTFL ..T.....G.....G.....A.....T.....G..... 484
 DNAPTTHA..G.C.....G.....CC..... 490

MAJORITY TCACCCCGCGGTGGCTTGGAGAACTACGGCCTGAGGCGGAGCGAGTGGGTGGACTACCGGGCGCTGGC

DNAPTAQG.....A.....C.....C.....CC.....A..... 557
 DNAPTFLAG.....C.G..... 554
 DNAPTTHA.....C.....T...C.....C..T 560

MAJORITY GGGGAGCCCTCGGACAACTCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG

DNAPTAQ C.....GAG.....T.....G..GAG.....T..GG.. 627
 DNAPTFLG..T...A.....G.....A..G.....A..CGC 624
 DNAPTTHT.....TC.....A.. 630

MAJORITY GAGTGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGCTGAAGCCCGC...CXTCGGGAGAGA

DNAPTAQGC.....C.....A..... 694
 DNAPTFLT..C..C.....A.....T..G.....C 691
 DNAPTTHA.....A.....A.AAA.G..... 700

FIG. 2C

MAJORITY [SEQ ID NO:7]	TCCAGGCCACATGGAXGACCTGAXGCTCTCCTGGAGGCTXTCGCAGGTGGCAGCCGACCTGCCCTGGA	
DNAPTAQ [SEQ ID NO:1]C..T.....A.....G..GG..A.....	764
DNAPTFL [SEQ ID NO:2]GGG.....G..G.....GCC..T.....C..A.....T.....A.....	761
DNAPTTH [SEQ ID NO:3]A.....C.....A.....C..G.....T.....C.....G.....C.....	770
MAJORITY	GGTGGAGCTTGGCGAAGXGGGGGAGGGCGGAGCGGGGCTTAAGGGCTTCTGGAGAGGCTGGAGTTT	
DNAPTAQAA.....A.....A.....T.....T.....	834
DNAPTFLGG..G..G..C..C..CACA..A..T.....T..GG.....T.....C..T.....	831
DNAPTTHC.....G..G.....G.....G.....G.....G.....	840
MAJORITY	GGCAGCCTCCTCCAGGAGTTCGGCCTCCTGGAGGGCGCCCAAGGCCCTGGAGGAGGCCCTGGCCCGCGC	
DNAPTAQT.....AA.....	904
DNAPTFLA.....G.....G..G.....GGCA.....T.....	901
DNAPTTHG.....G.....G.....G.....G.....	910
MAJORITY	CGGAAGGGCCCTTCGTGGCTTGTCTTCGGGGCGGAGGCCATGTGGCGCGAGCTTCTGGCCCTGGC	
DNAPTAQG.....AAG.....T.....	974
DNAPTFLT..T.....TC..T.....T.....AAA.....	971
DNAPTTHC.....C.....G.....	980
MAJORITY	CGCGGCGCAGGGAGGGCGGCTCCAGCGGGCAGCAGCCCTTAXGGGGCTXAGGGAGCTXAAGGAGGTG	
DNAPTAQG.....G..C..G..T..A..AA..G..G.....G.....C..	1044
DNAPTFL	T..GG..GT.....G..GG.....T.....A.....G.....G.....T.....G.....	1041
DNAPTTHTG.....C.....G.....G.....G..G..G..A..A.....C.....C.....	1050

Age Group	Percentage of Respondents
18-29	85
30-49	75
50-69	65
70+	55

FIG. 2E

MAJORITY [SEQ ID NO:71]	GGAGATCGCGCGCTCGAGGAGGCTTCGGCGTGGGGGGGAGCCCTTCAAGCTCAAGTCCCGGGAG	
DNAPTAQ [SEQ ID NO:1]GC.....CC.....	1484
DNAPTFL [SEQ ID NO:2]	...G.G...AG..G.....	1481
DNAPTTH [SEQ ID NO:3]T.....G.....	1470
MAJORITY	CAGCTGGAAAGGCTGCTCTTTCAGGAGCTXGGGCTTCGGCGCATCGGCAAGACGGAGAGCXGGCAAGC	
DNAPTAQC.....A.....	1534
DNAPTFLGC.....G..G..T.....	1531
DNAPTTHTA.....T.G..G.....C.A.....A.....	1540
MAJORITY	GCTCCAGCAGCGCGCGCTGCTGGAGGCGCTXCGXGAGGCGCCCATCGTGGAGAGATCCTGCAGTA	
DNAPTAQC.....C..C.....	1604
DNAPTFLT.....G..A.....CCC.....	1601
DNAPTTHG.....A..G.....C.....C.....C.....	1610
MAJORITY	CGGGAGCTCAGCAAGCTCAAGAACAGCTAGATXGAGCGCGCTGGCXGXGCTGGTGGAGCGCAGGAGGGG	
DNAPTAQB.....T.....G.A...A.....	1674
DNAPTFLA.....C.C...G.....A...C...	1671
DNAPTTHG.G.....C..AAG.....G.....	1680
MAJORITY	CGCGTCCACACCGCGCTTCAACGAGACGGCCAGCGCGCAGGCTTAGTGGTCCGAGCGCAGCCTGC	
DNAPTAQA.....T.....C.....	1744
DNAPTFL	..G.....C.....TCG.....	1741
DNAPTTHG.....	1750

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAACATCGCCGTCGCCACGCCXCTGGGCGAGGATCGGGCGGCGCTTCGTGGCCGAGGAGGGGTGGGT	
DNAPTAQ [SEQ ID NO:1]G..T..G.....A..C.....G...C.	1814
DNAPTFL [SEQ ID NO:2]G.....T.....C..C.....A.....C.....	1811
DNAPTTH [SEQ ID NO:3]CT.....T.....G...T...C	1820
MAJORITY	GTTCGTGGCCCTGGACTATAGCCAGATAGAGCTCGGGGTCTGGCCGAGGCTCTCCGGGAGGAGAGGCTG	
DNAPTAQ	A.....A.....A.....A.....G.....C.....	1884
DNAPTFL	.C.....T..T.....C.....T.....T.....T.....	1881
DNAPTTHC.....C.....C.....C.....A.....	1890
MAJORITY	ATCCGGGTCTTCAGGAGGGAGGGAGATCCACAGCCAGAGGGGAGGCTGGATGTTCCGGCTCCCGCCGG	
DNAPTAQC.....GG.....G.....G.....G...	1954
DNAPTFLT.....T.....T.....T.....T.....C.	1951
DNAPTTH	...A.....A.....A.....A.....A.....	1960
MAJORITY	AGCCGCTGGACCCCTGATGCCCGGGGGCCAGACCAACATCAACTTCGGGGTCCCTCTAGGGGATGTCGGG	
DNAPTAQA.....A.....A.....A.....A.....G...	2024
DNAPTFL	.A.GG..A...T.....T.....G.....G.....	2021
DNAPTTHGG.G.....C.....C.....C.....	2030
MAJORITY	CCACCGGCTCTCCGAGGAGCTTGGCATCGGCTACGAGGAGGGGTTGGCCCTTCATTGAGGGCTACTTCAG	
DNAPTAQA.....T.....CCA.....T.....	2094
DNAPTFLGG.....T.....T.....T.....	2091
DNAPTTH	...TA.G.....T.....T.....A.....A	2100

FIG. 2G

MAJORITY [SEQ ID NO:73]	AGCTTCGCCAAGGTGGGGGCTGGATTGAGAAAGACCGCTGGAGGAGGCGGCGGCTAGCTGGAGA	
DNAPTAQ [SEQ ID NO:13]	2164
DNAPTFL [SEQ ID NO:21]	...A.....GG.....C.CC.....T.....	2161
DNAPTTR [SEQ ID NO:31]A.A.....G.....A.....C.....A.	2170
MAJORITY	CCCTCTTCGGCCGCGGGGCTACGTGCCGGACCTCAAGCGCGCGGGTGAAGAGCGTGGGGAGGCGGCGGA	
DNAPTAQC.....A.....AG.G.....C..	2234
DNAPTFLT.....C.....	2231
DNAPTTRAA.AA.....CA.....C.....	2240
MAJORITY	GGGCATGGCCTTCAACATGGCGGTCCAGGGCAGCGCGCGGACCTCATGAAGTGGGCATGGTGAAGCTG	
DNAPTAQ	2304
DNAPTFLG.....T.....CG...T	2301
DNAPTTRC.....C.....	2310
MAJORITY	TTCCGCCGGCTXCAAGAAATGGGGGCCAGGATGGTGGTCAAGGTCCAGGAGGAGCTGGTGGTGGAGGCGG	
DNAPTAQA...GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTRG..C.G..B.....C.C.....C.....CC...G.....	2380
MAJORITY	CCAAAGAGCGGGCGGAGGXGGTGGCGGCTTTGGCCAGGAGGTCATGGAGGGGGTCTATCCCTGGCCGT	
DNAPTAQA.....CC.....CGGC.....G.....	2444
DNAPTFLG..C.....AG...A.....GG.....CAG..	2441
DNAPTTRC...C.....C...A.....G.....AA..C.....C.....	2450

FIG. 2H

MAJORITY [SEQ ID NO:7]	G G C C C T G G A G G T G G A G G T G G G G A T G G G G A G G A C T G G C T C T C G G G C C A A G G A G T A G	
DNAPTAQ [SEQ ID NO:1]A.....	GA 2499
DNAPTFL [SEQ ID NO:2]CC.....	2496
DNAPTTH [SEQ ID NO:3]T.....	GT... 2505

FIG. 3A

MAJORITY	[SEQ ID NO: 8]	MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUOAVYGFASLLKALKEDG·DAVXVVVFDK	
TAQ PRO	[SEQ ID NO: 4]	RG.....H.....	69
TFL PRO	[SEQ ID NO: 5]V.V.....	68
TTM PRO	[SEQ ID NO: 6]YK..F.....	70
MAJORITY		APSRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPQYEADDVLATLAKKAKEGYEVRIL	
TAQ PRO		68.....A.....S.....	139
TFL PRO	V.....F.....R.....	138
TTM PRO	FT.....	140
MAJORITY		TADRDLQLSDRIAVLHPGYLITPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKSIGEKTXKLLX	
TAQ PRO		K.....H.....D.A.....T..E.....R...E	209
TFL PRO	E...I.....Y.....A.....I.....QR..R	208
TTM PRO	V...V.....H...E.....F...V.....L...K	210
MAJORITY		EWGLENLLKNLDRVKP·XXREKIXAHMEDLXLSSXLSXVRTDLPLEVDFAXRREPDRBGLRAFLERLEF	
TAQ PRO		A.....L...AI...L...D...K..WD.AK.....K.....R.....	278
TFL PRO		FOH...Q...SL...LQ.G..A.A..RK..O.H.....GR..T.NL.....	277
TTM PRO		ENV...K..L...R..LE..R.....L.QG.....	280
MAJORITY		GSLLEFGLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEELLALAAARXGRVHRAXDPLXGLRDLKEV	
TAQ PRO		S.....S.....K.....D.....G.....PE.YKA.....A	348
TFL PRO		G...A.....L..SF.....G.WE..L...O...R.....G.	347
TTM PRO		A.AP.....A.....K.....G.D.....A...A..K.....	350

FIG. 3B

MAJORITY [SEQ ID NO: 8]		RGLLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTE DAGERALLSERLFXNLXX	
TAQ PRO	[SEQ ID NO: 4]	S.....G.P.....	E.....A.....A...WG 418
TFL PRO	[SEQ ID NO: 5]	I.....F.E.....	A.....QT...KE 417
TTH PRO	[SEQ ID NO: 6]	S.....V.....	AH.....HR...LK 420
MAJORITY		RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEI RRLEEEVFRLAGHPFHLNSRD	
TAQ PRO		R...R...A.....R.....A.....A.....	488
TFL PRO		K.....E.....R.....EA.V.Q.....	487
TTH PRO		K.....H.....L.....	490
MAJORITY		QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PRO	S.....D.I.....	558
TFL PRO	DR.....A.....K...	557
TTH PRO		R...L...Q.....H.....V.....S.....	560
MAJORITY		RLHTRFNOTATATGRSSSDPNLONI PVRTPLGQRIRRAFVAEEGHWXLVALDYSDIELRVLAHLSGDENL	
TAQ PRO	I.....L.....	628
TFL PRO	V...V.....	627
TTH PRO	A...A.....	630
MAJORITY		IRVFQEGRDIHTQTASWMF GVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSDELAI PYEEAVAFIERYFQ	
TAQ PRO	E.....R.....Q.....	698
TFL PRO	S...G.....G...S.....	697
TTH PRO	K.....V.....	700

TAP PRO	E.	E.	A.	R.	.	.	.	L.		. . .	833
TFL PRG	O.	L.	.	.	.	D.	R.	.	.	W.	Q.	.	L.	.	831
TTH PRG	R.	L.	QA.	E.	.	A.	K.A.	.	M.	G	835

Genes for Wild-Type and Pol(-)DNAPTaq

Domain

Coding Regions: 5' Nuclease

Polymerase

FIG. 4A

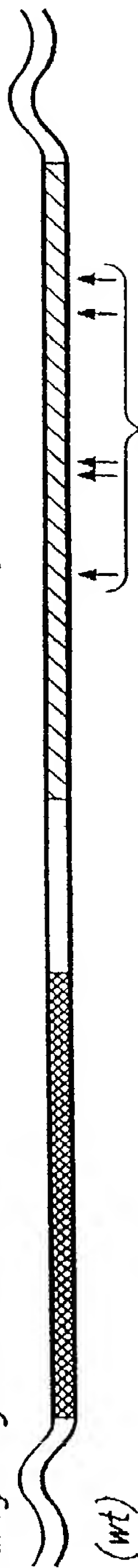


FIG. 4B

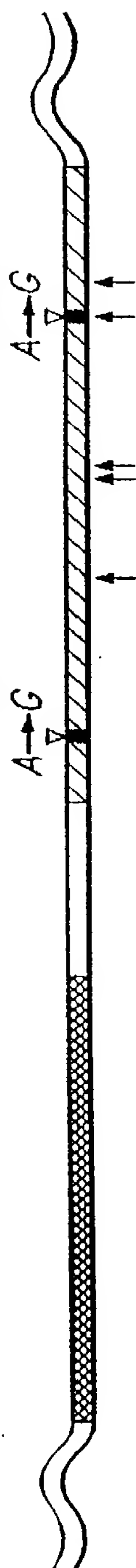


FIG. 4C



FIG. 4D

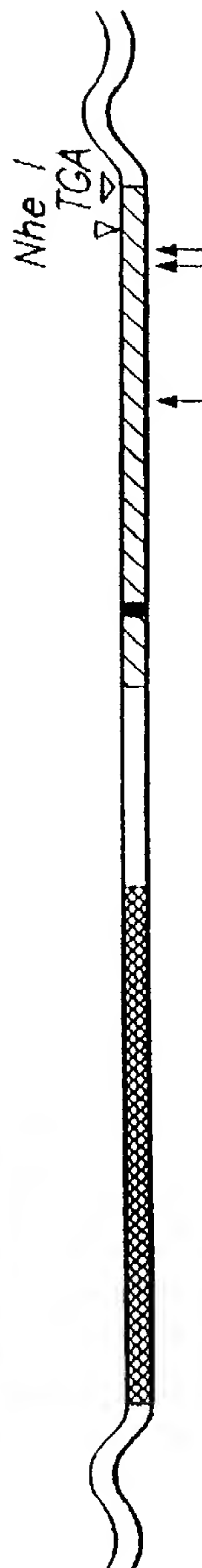


FIG. 4E



FIG. 4F

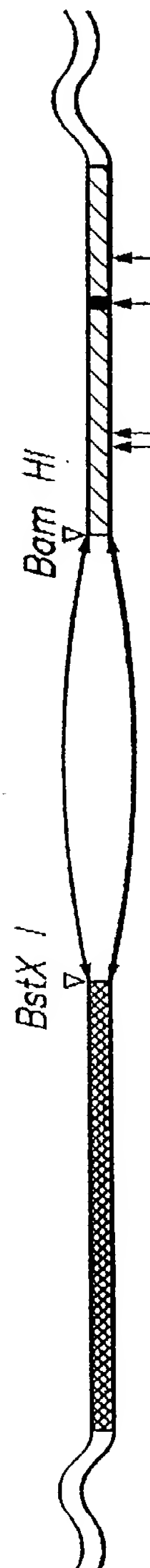
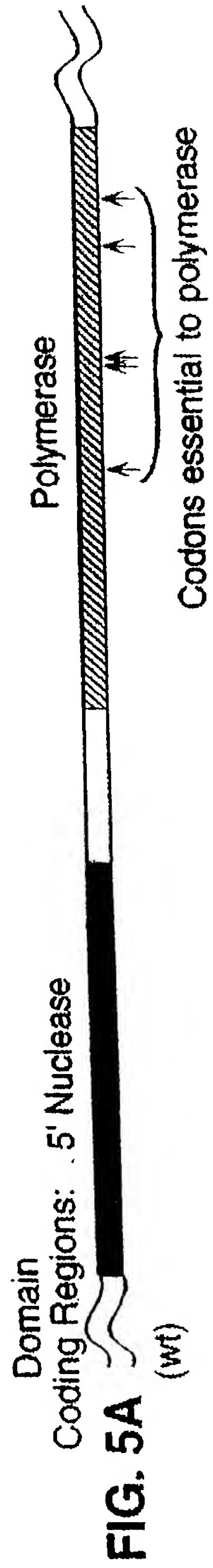


FIG. 4G



Genes for Wild-Type and Pol(-) DNAPTfl



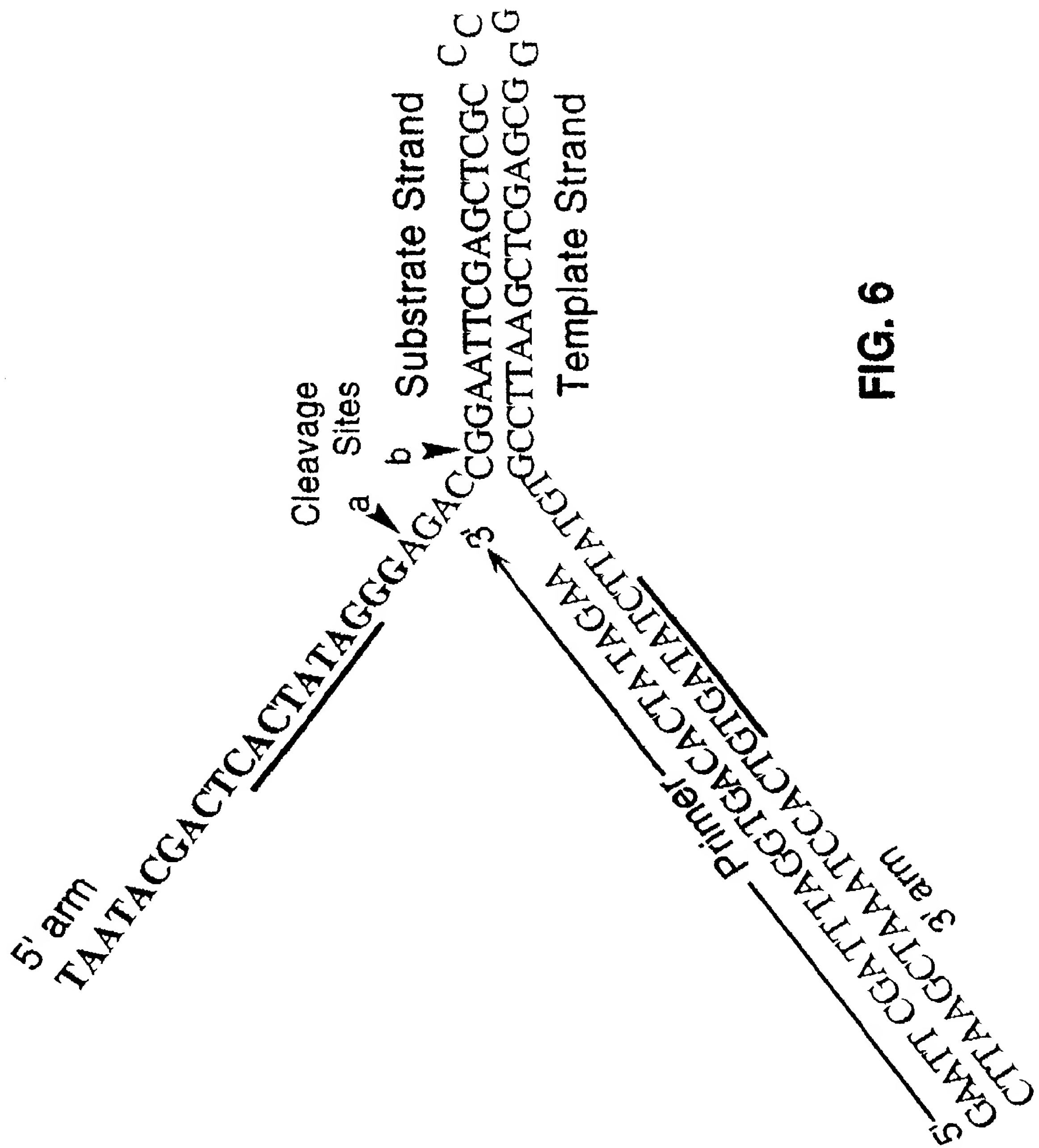


FIG. 6

DNAP	T		S		
TARGET					
DNA	M	- +	- +		M



FIG. 7

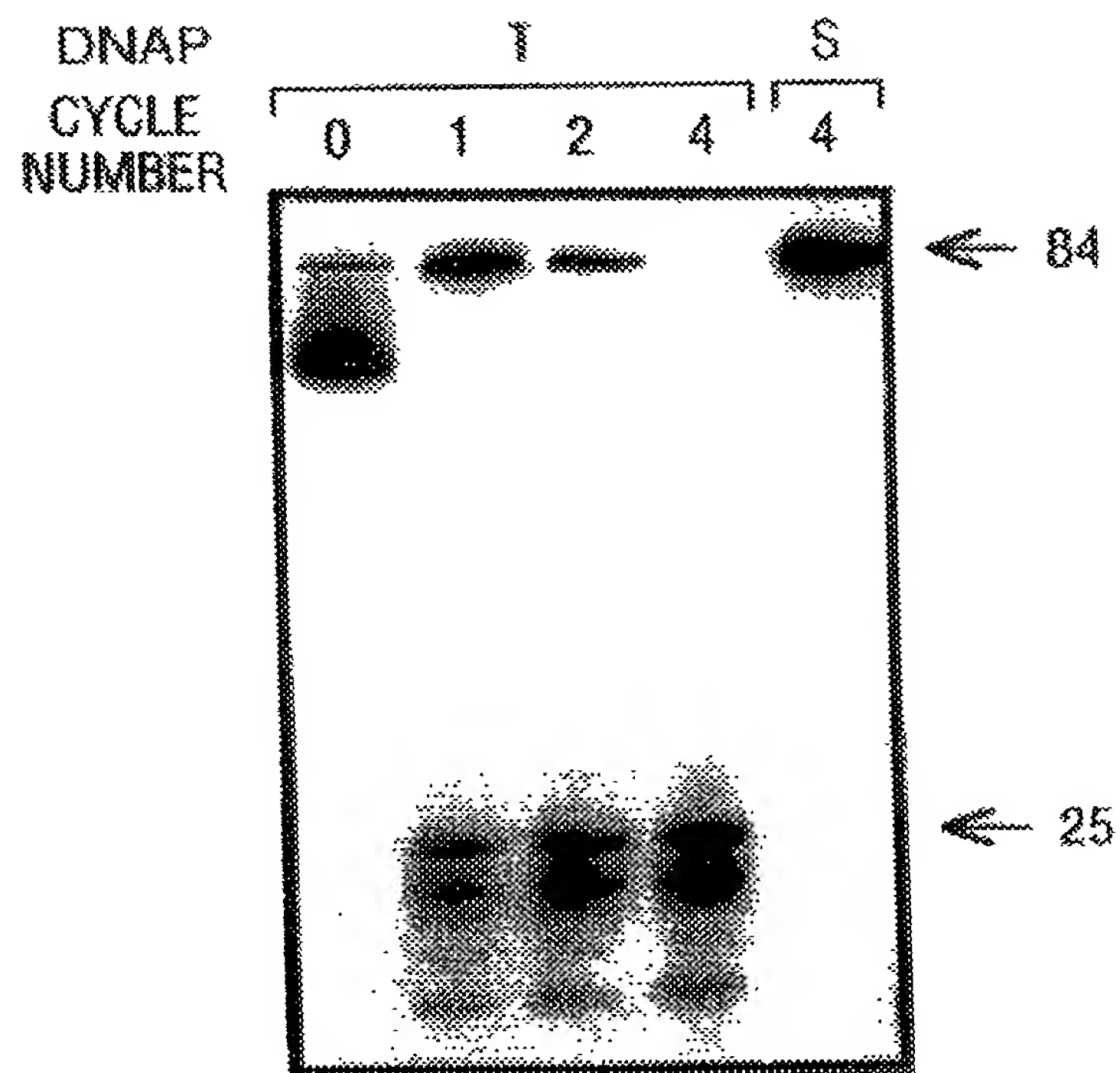
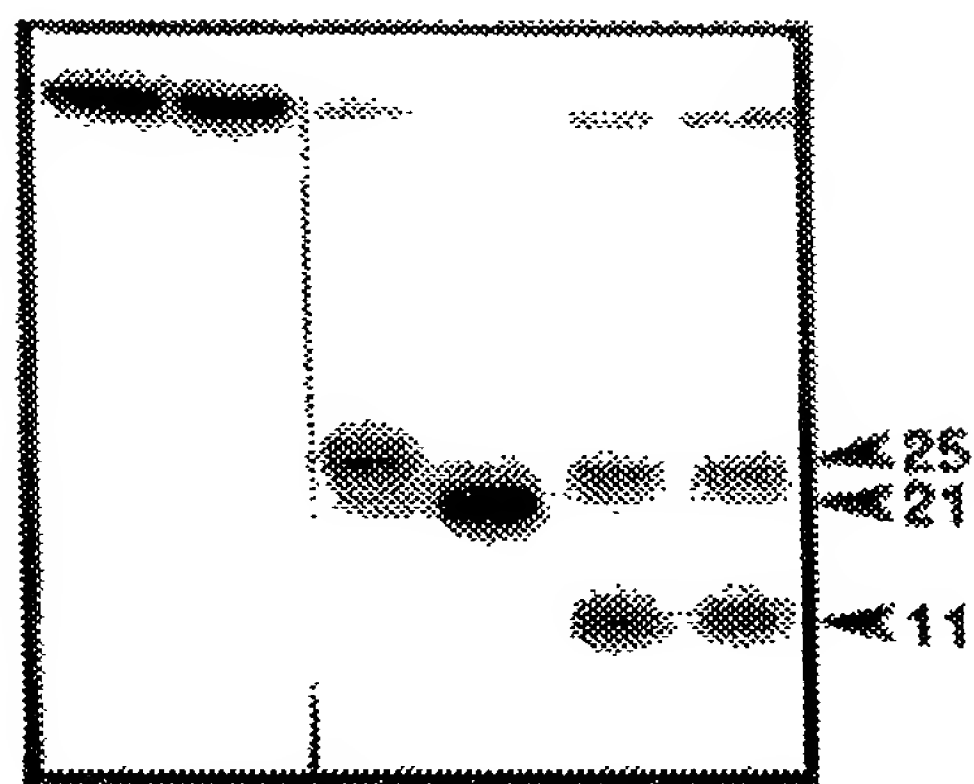


FIG. 8



°C: 0 37 55 72

25

11

FIG. 9B

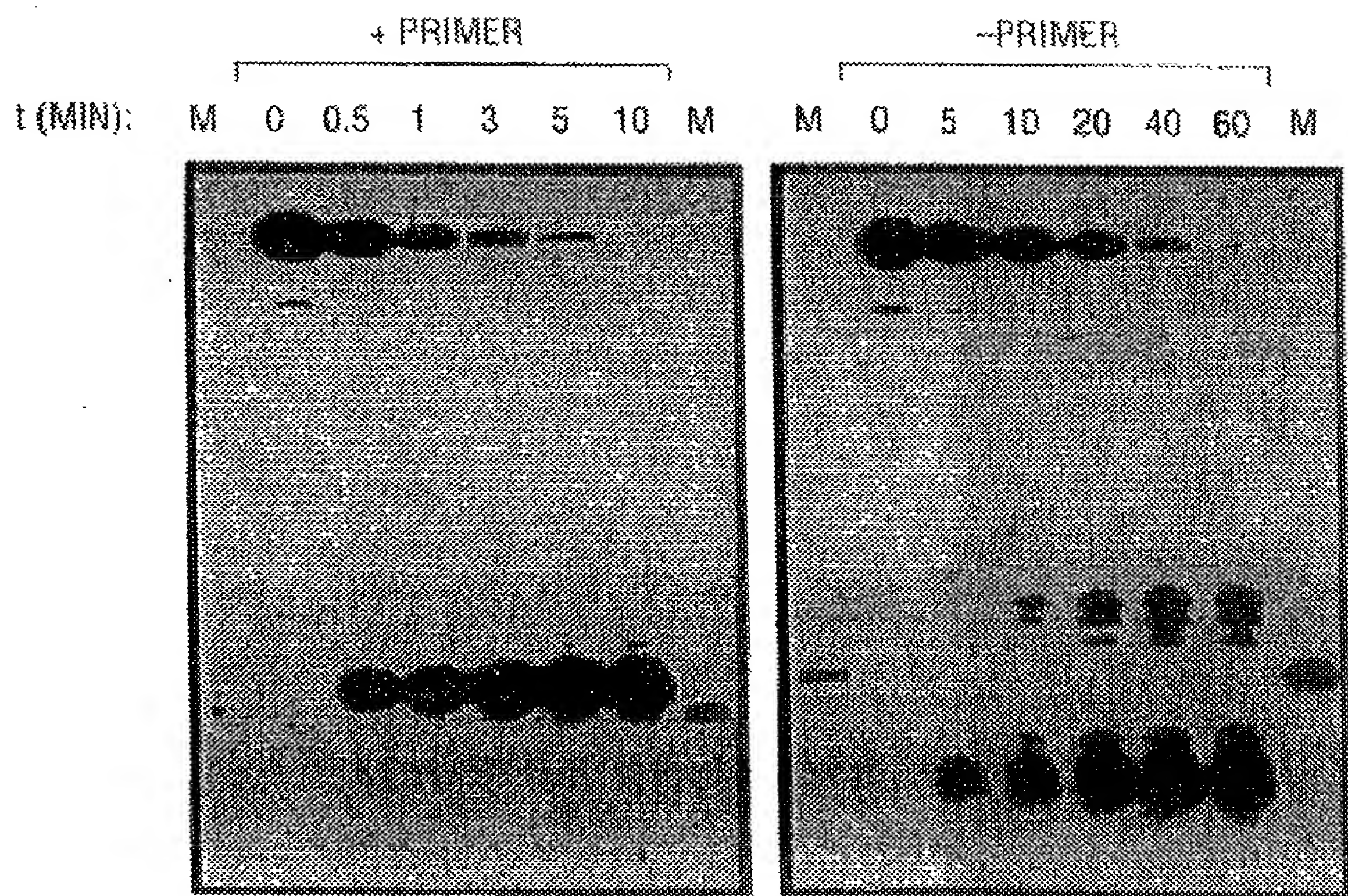


FIG. 10A

FIG. 10B

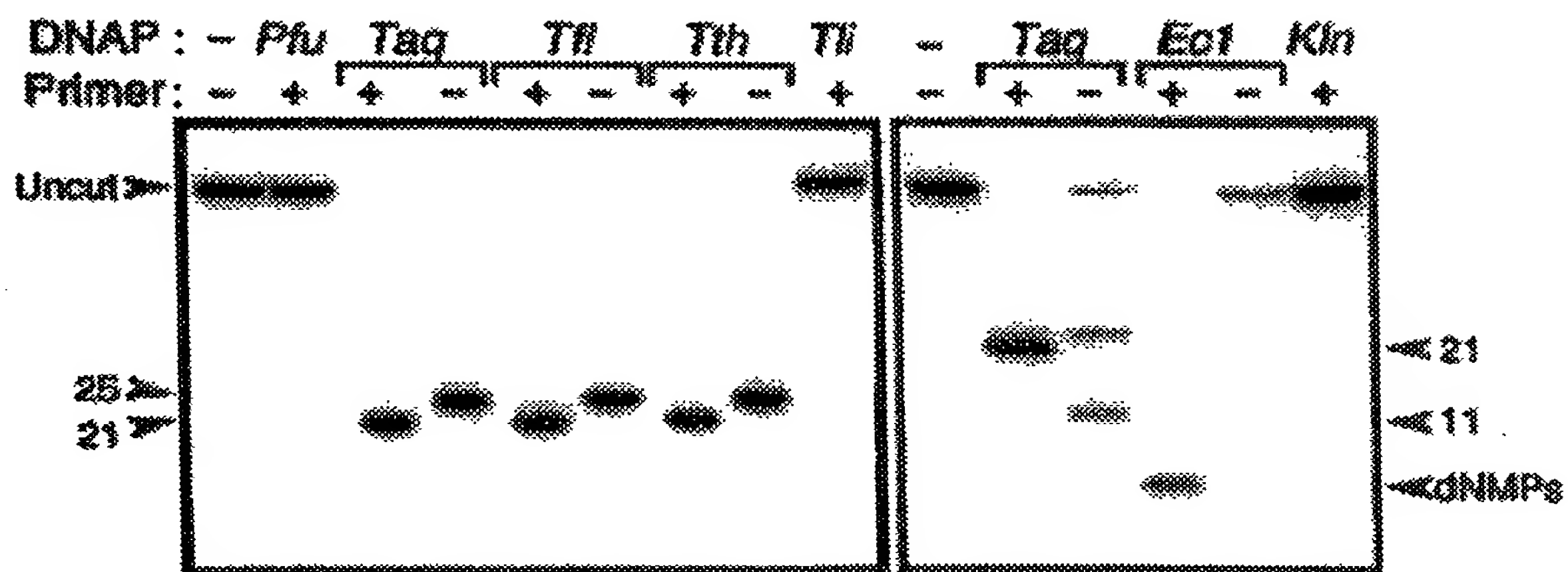
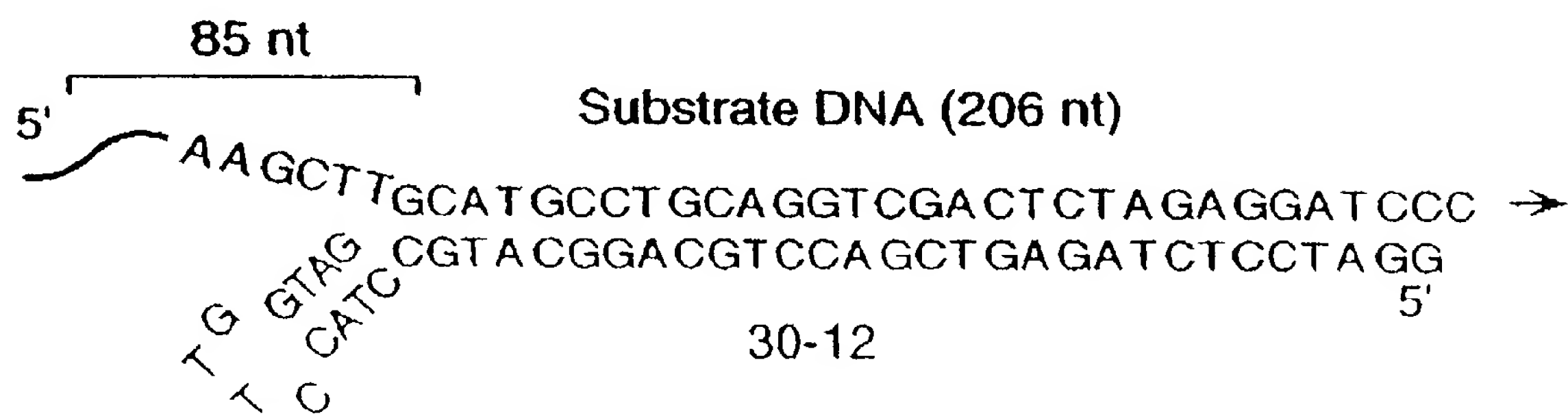
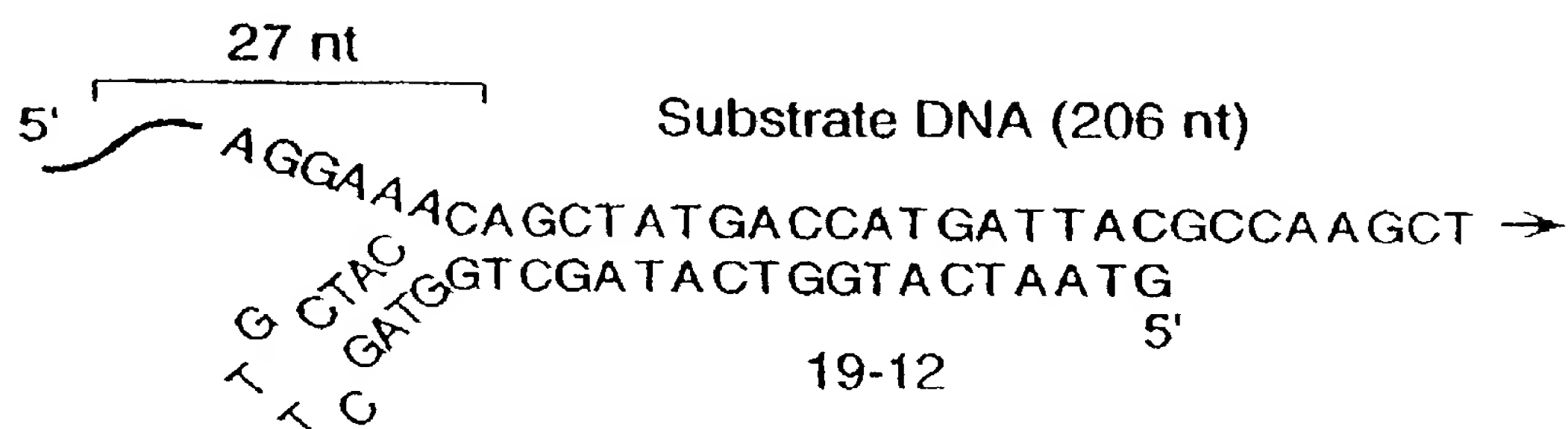


FIG. 11A

FIG. 11B

FIG. 12A



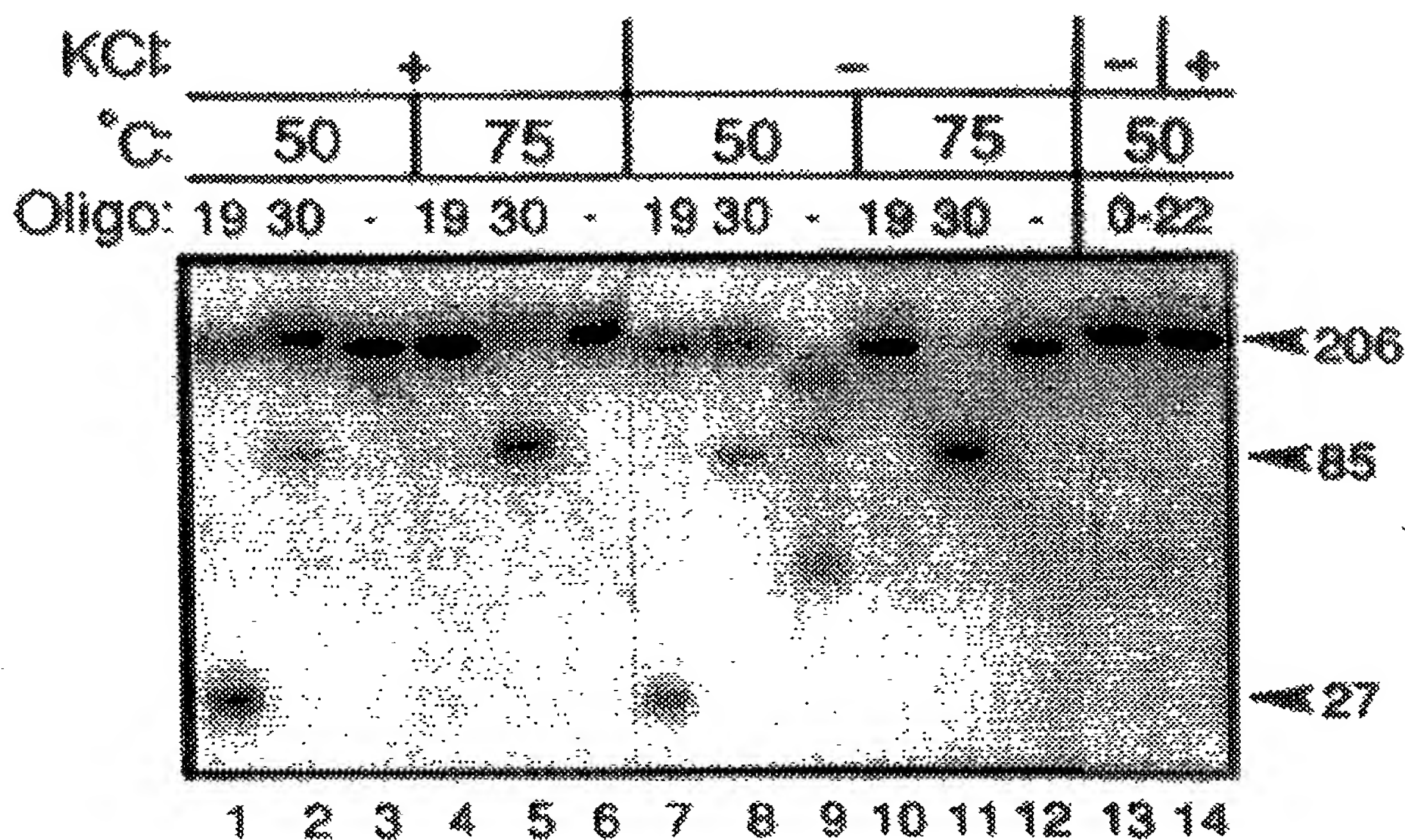


FIG. 12B

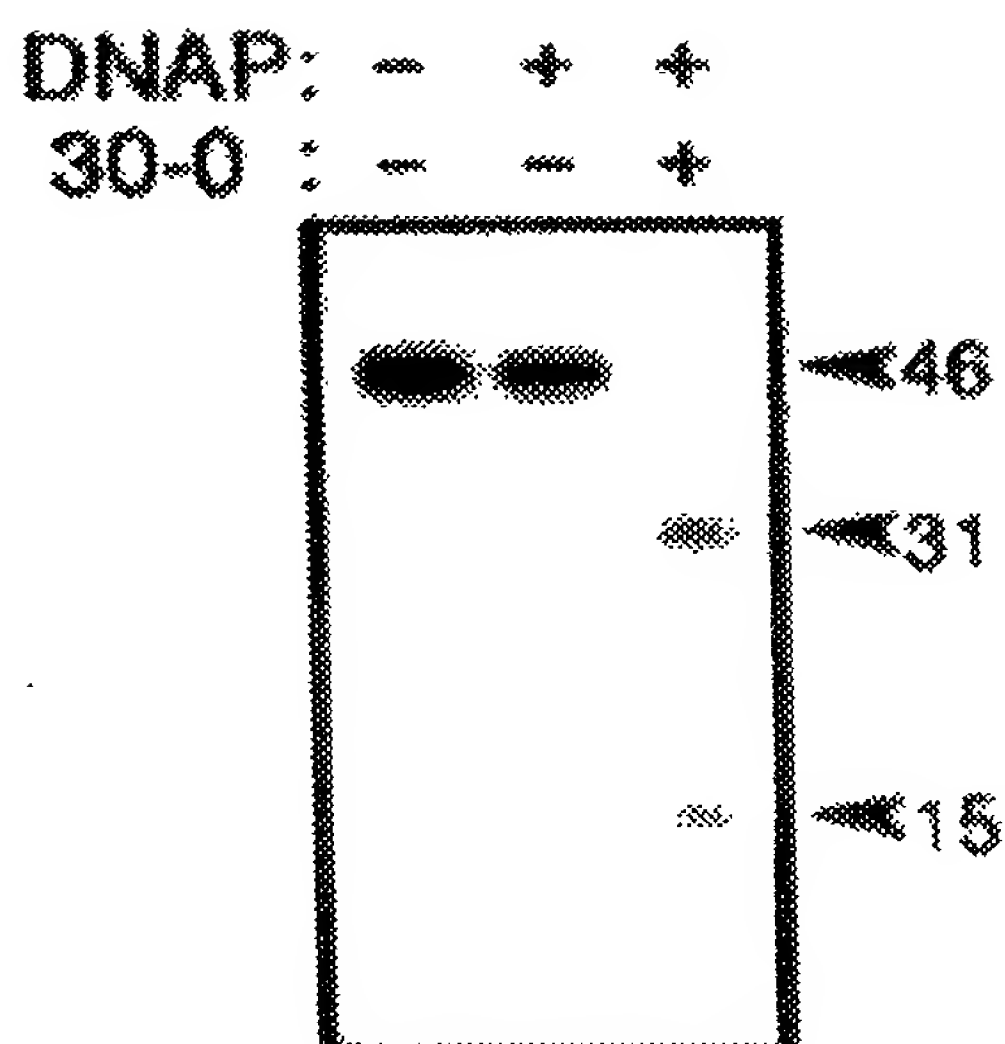


FIG. 13B

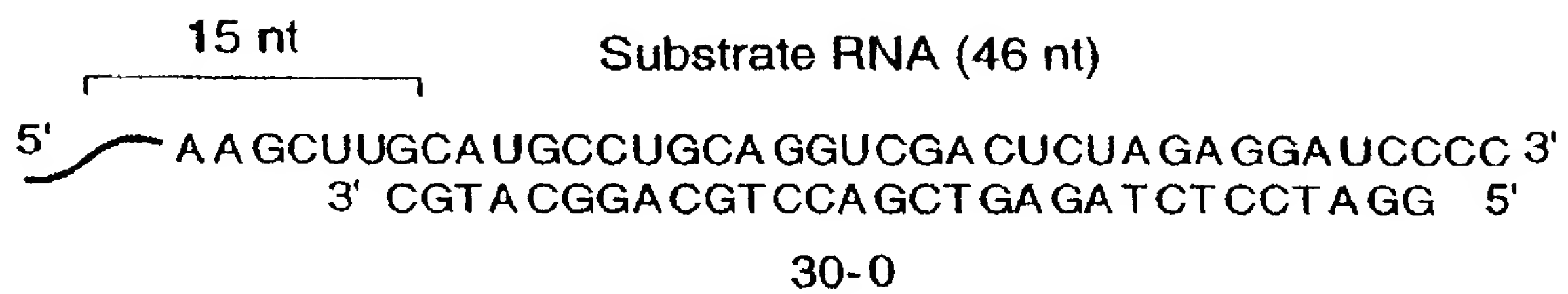
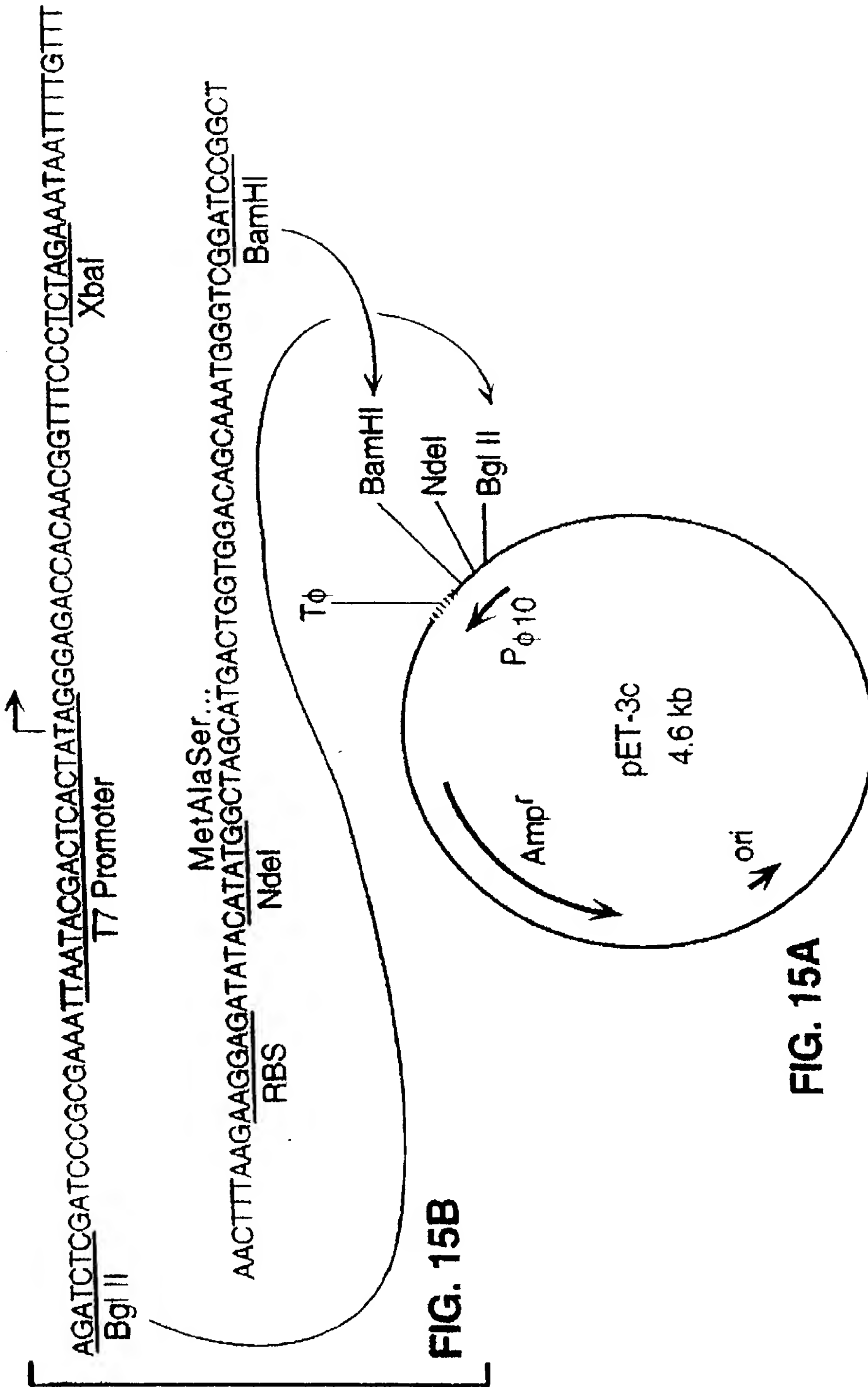
**FIG. 13A**



FIG. 14C



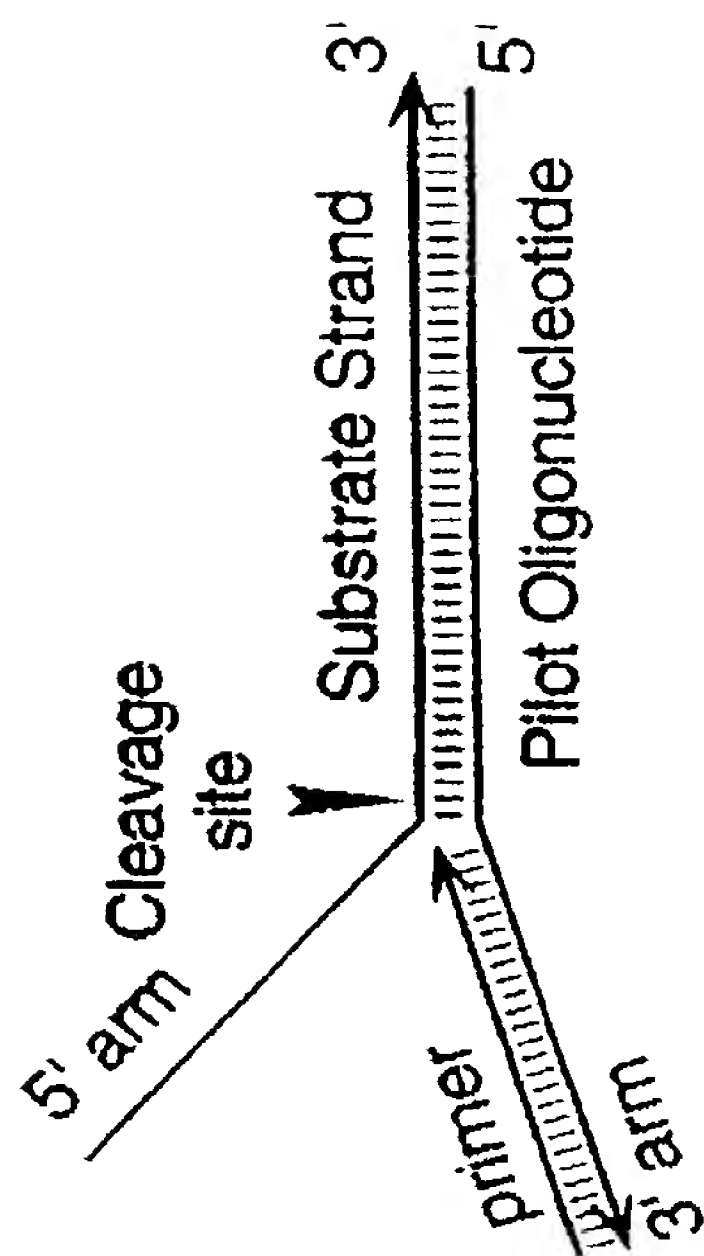


FIG. 16B

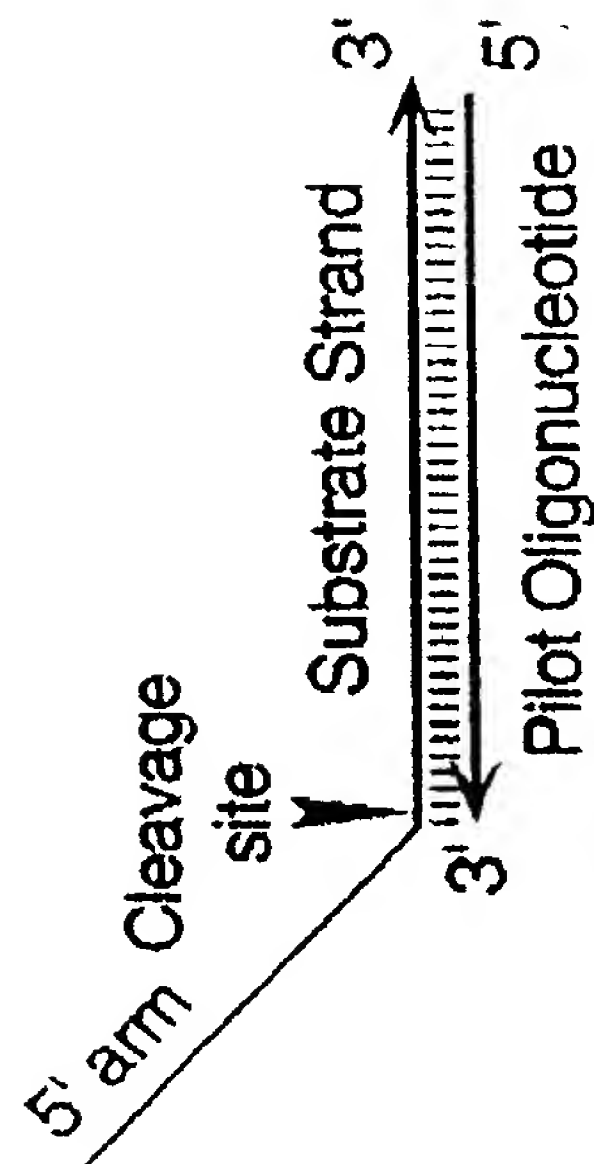


FIG. 16D

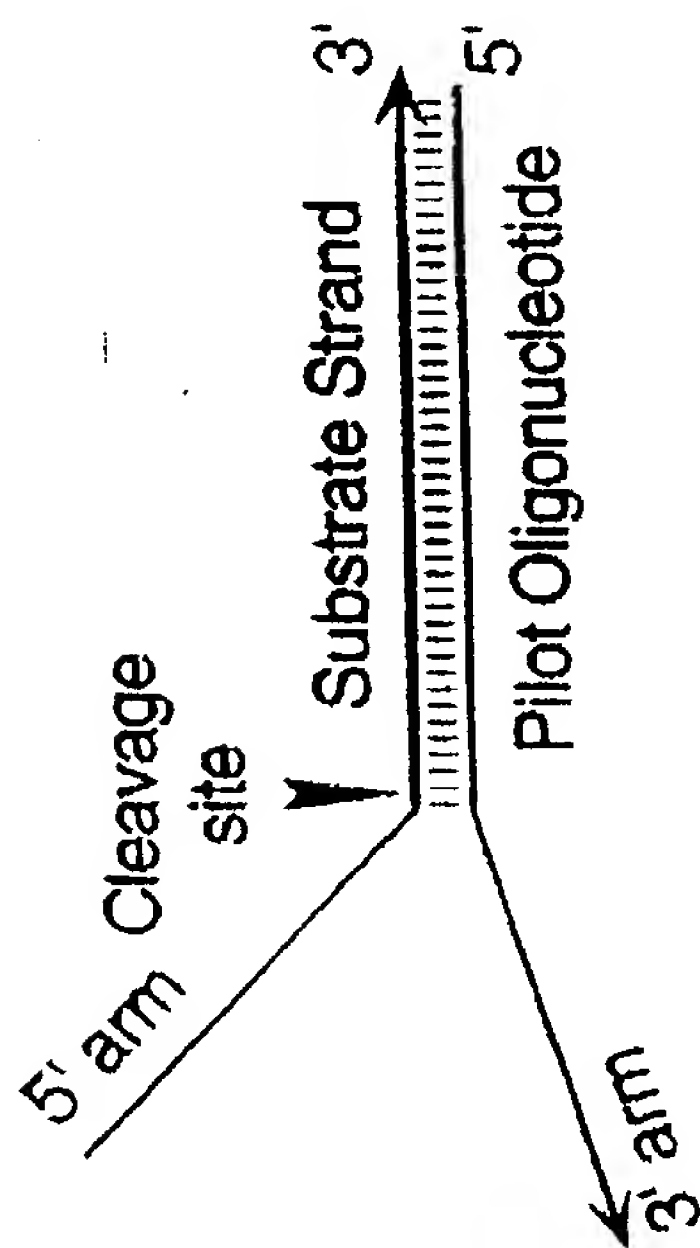


FIG. 16A

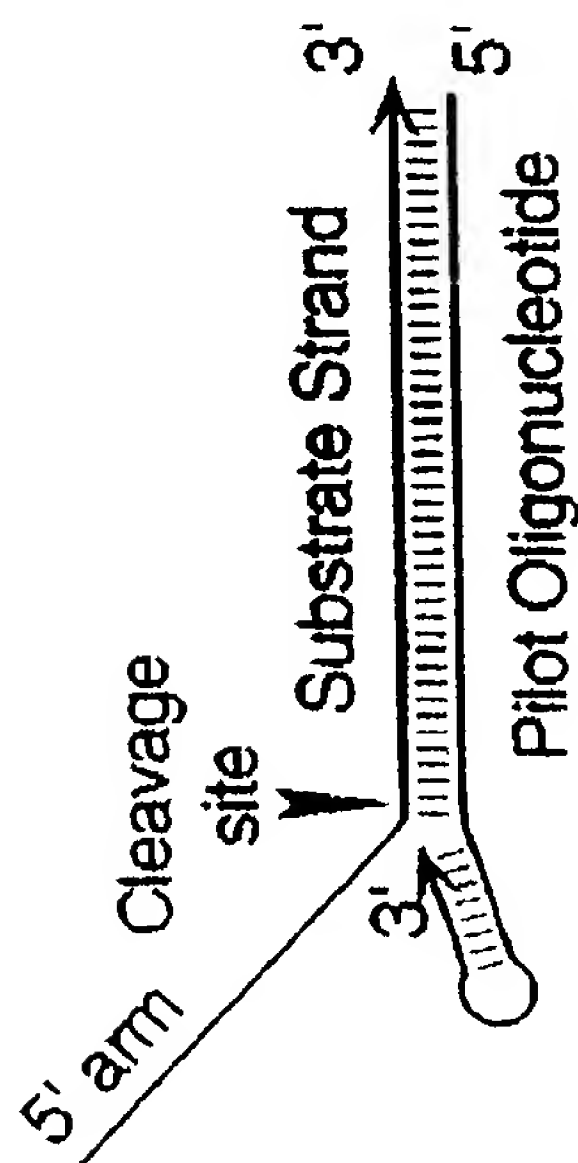


FIG. 16C

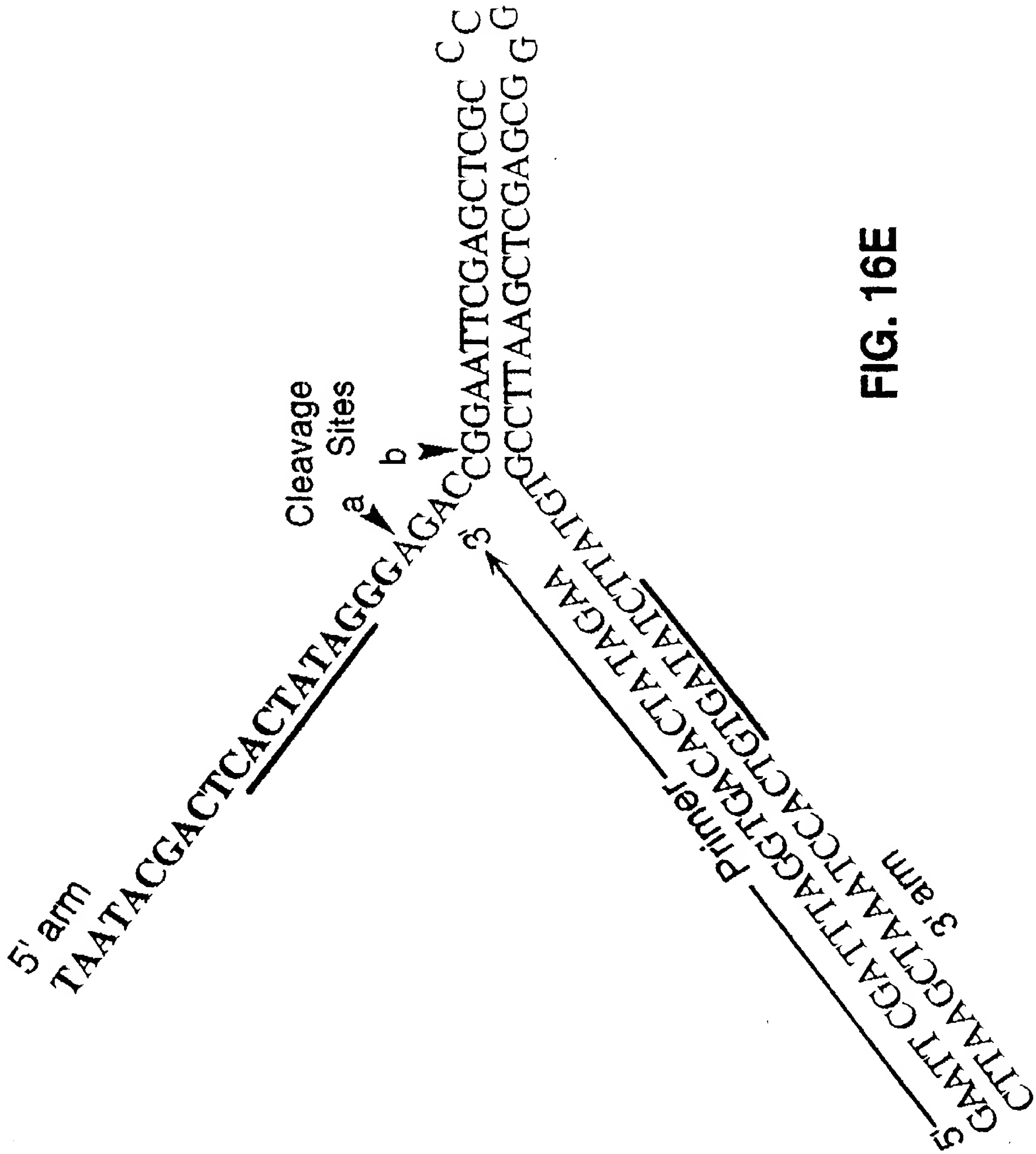


FIG. 16E

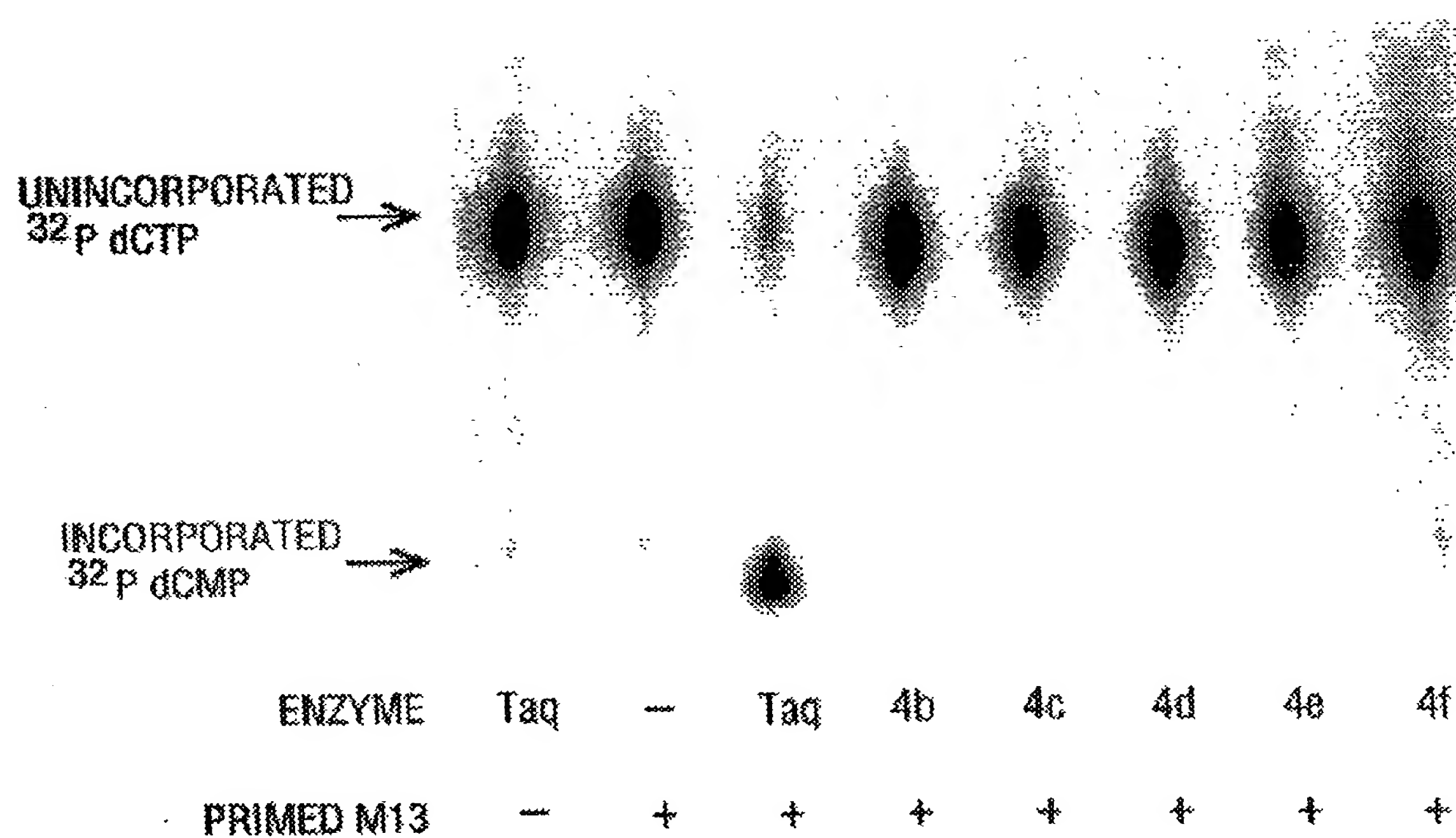


FIG. 18

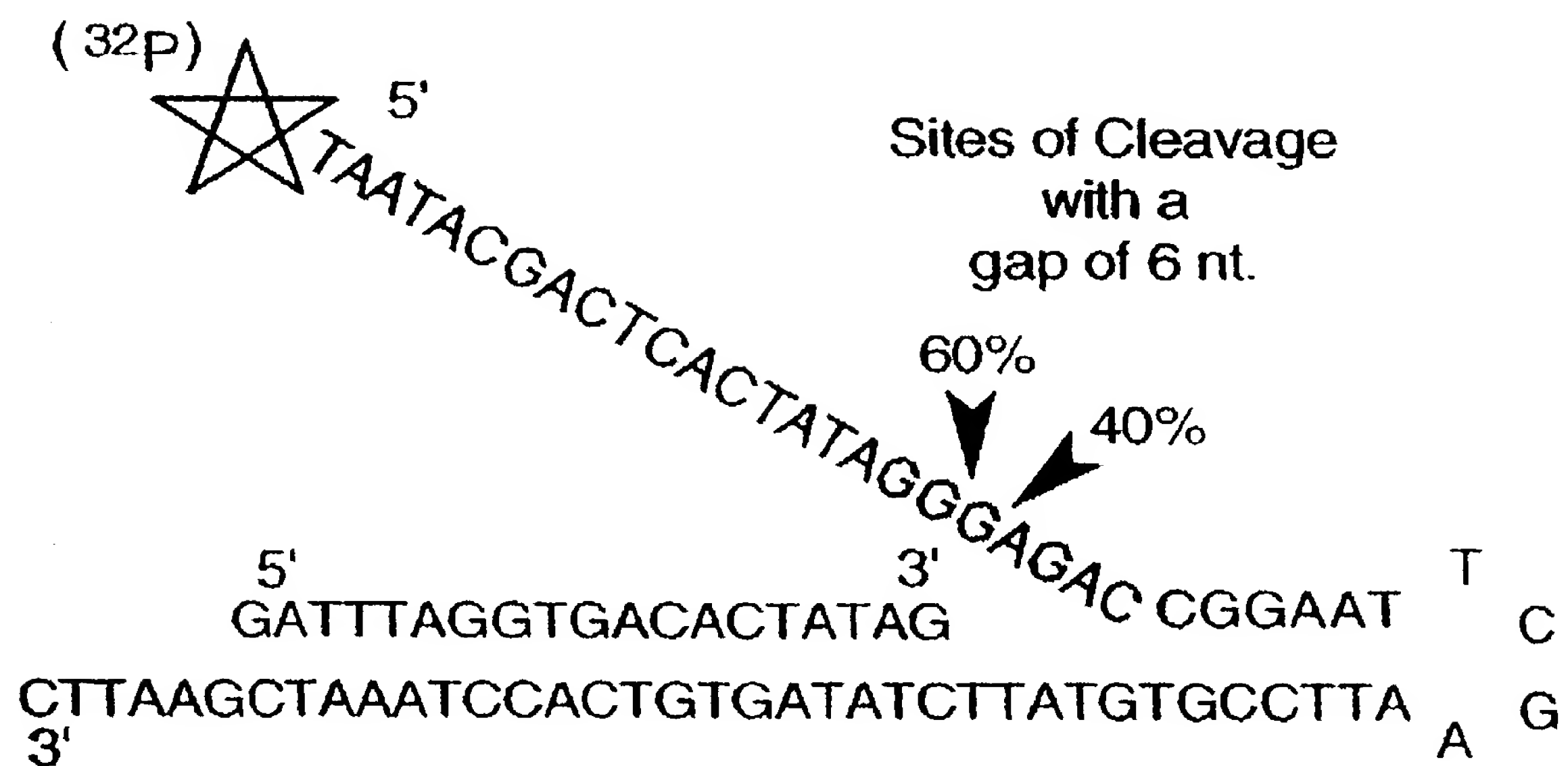


FIG. 19A

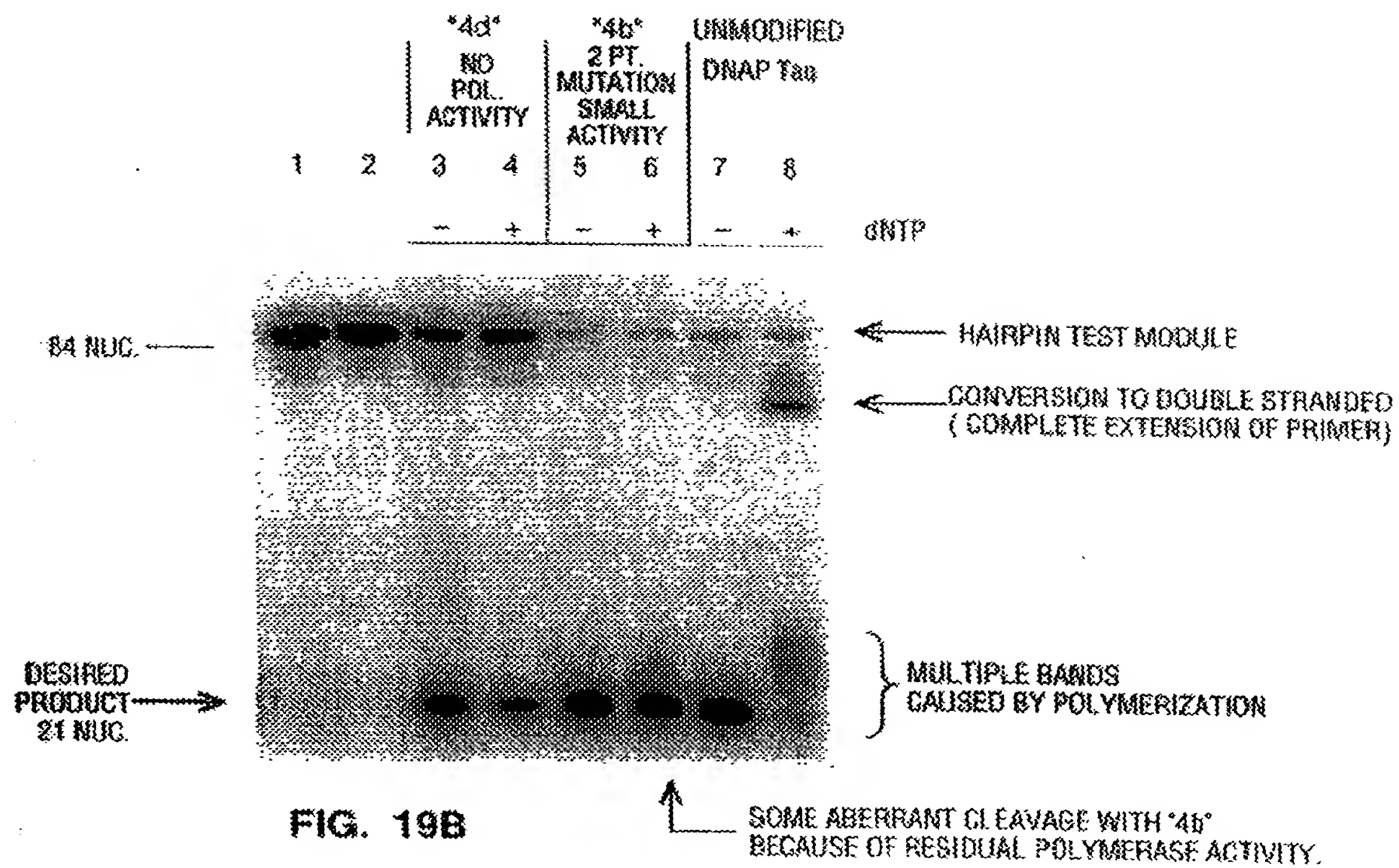


FIG. 19B

Sequence of alpha primer:
5' GACGAACAAGCGAGACAGCG 3'

FIG. 20C

Cleaved A-Hairpin

5' Tau primer 3' 5' ACACAG GTACC A C
CAAGACGACACAGCAGAGACGGAGAA CATGG T A

Cleaved T-Hairpin

5' Alpha primer 3' 5' CCTCTT GTACC A T
CTGCTTGTCGCTCTGCTGTGTC CATGG T G

FIG. 20D

FIG. 20D

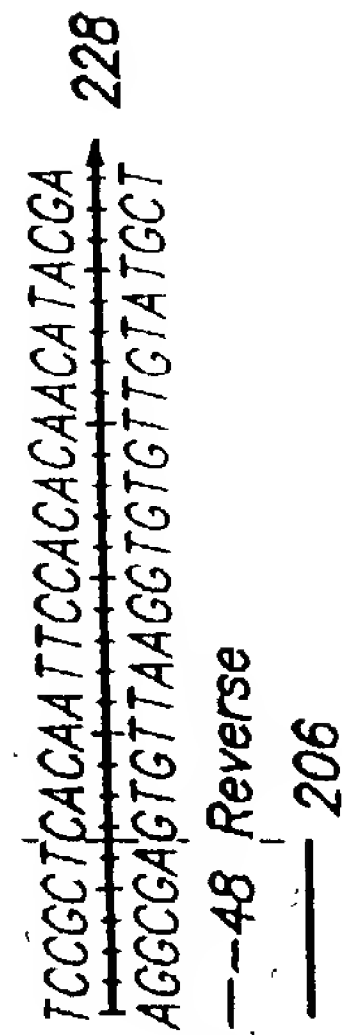
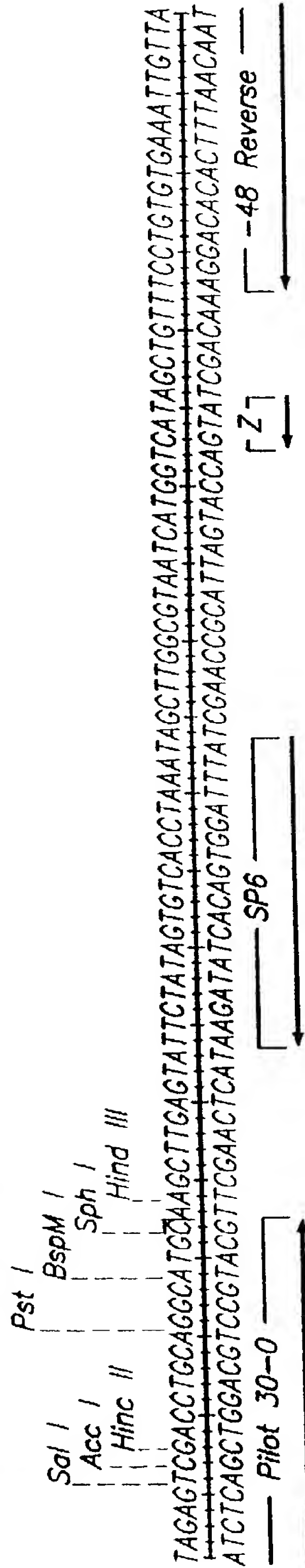
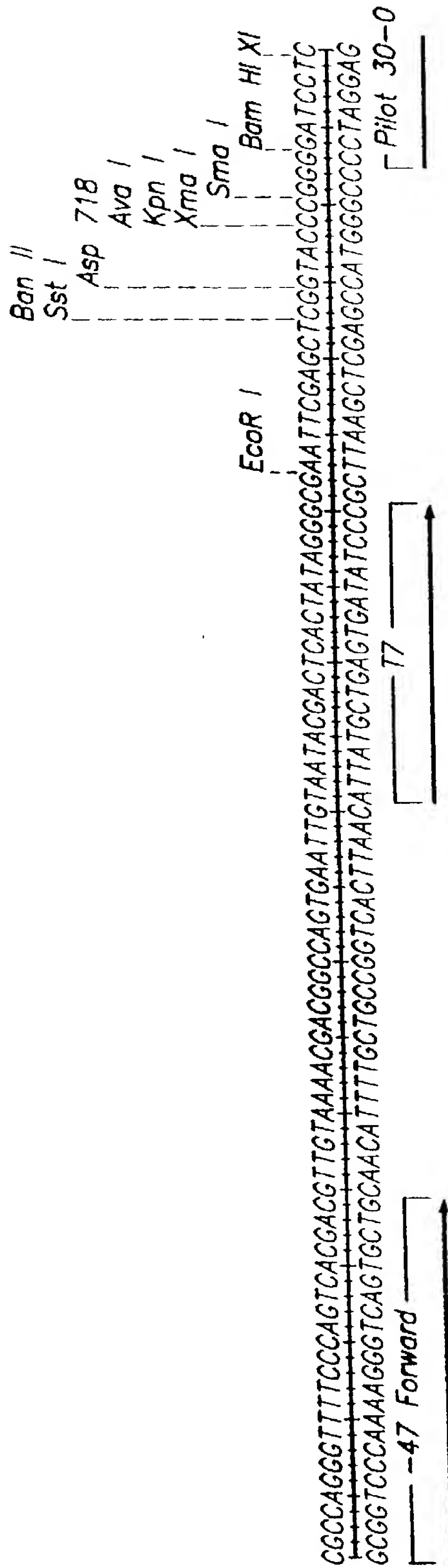


FIG. 21

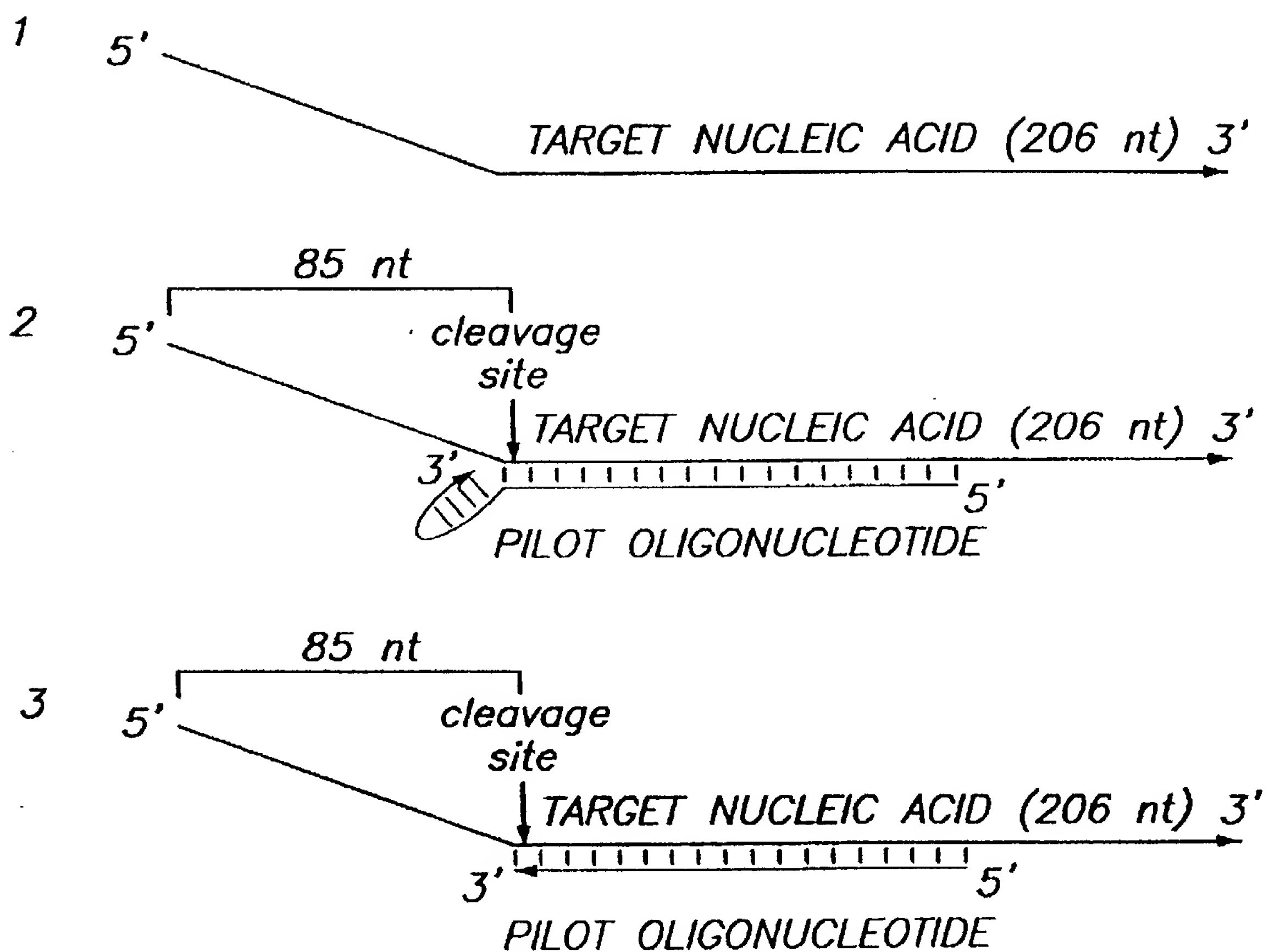


FIG. 22A

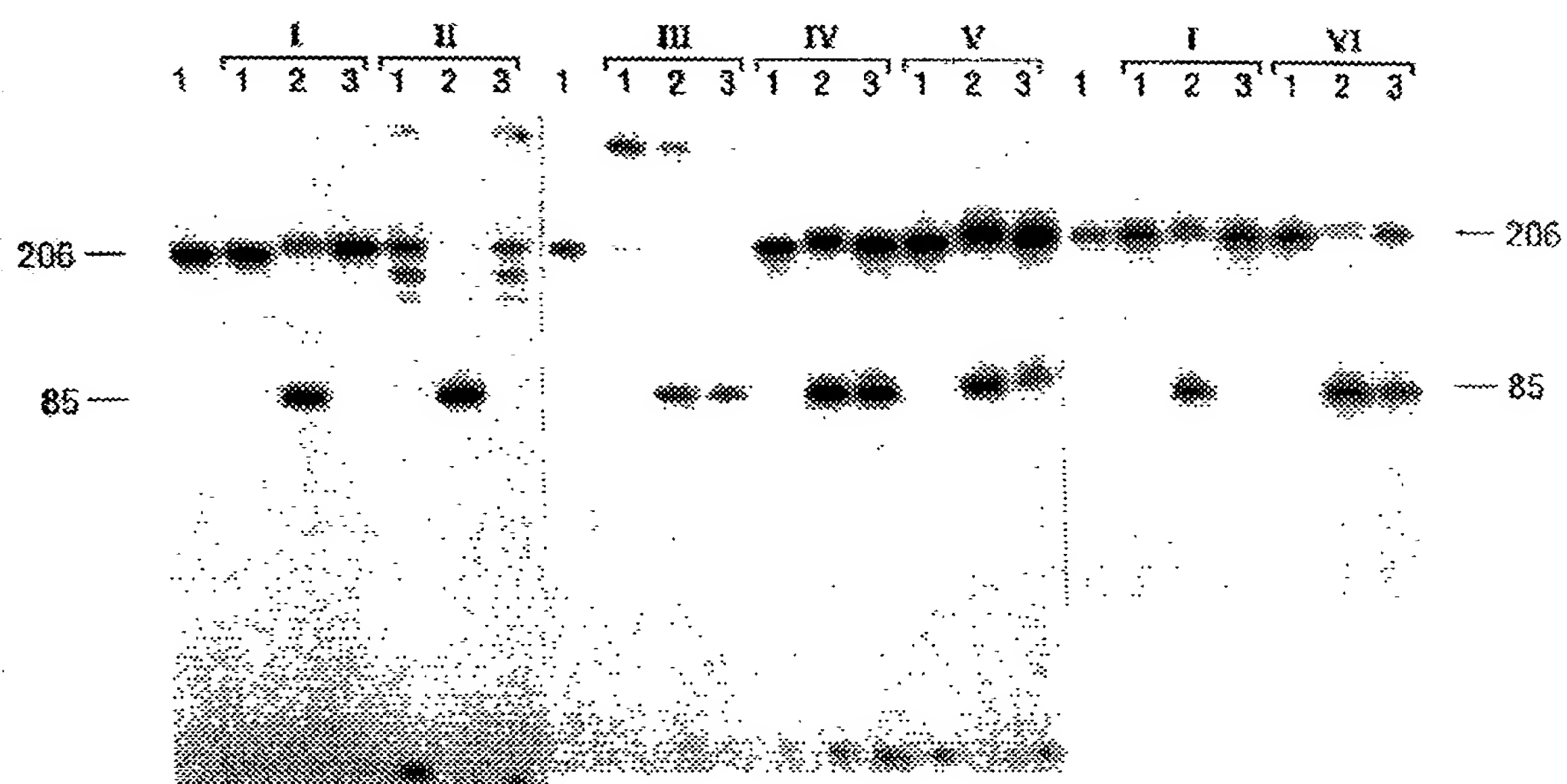


FIG. 22B

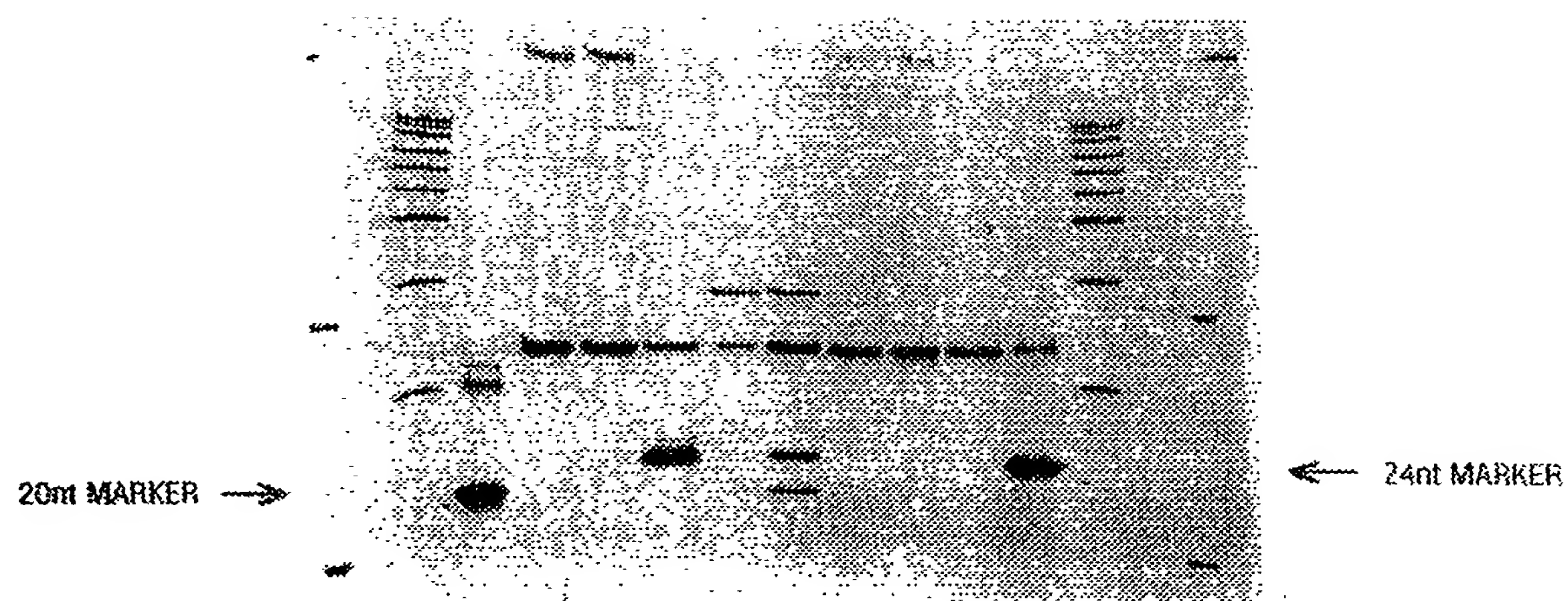


FIG. 24

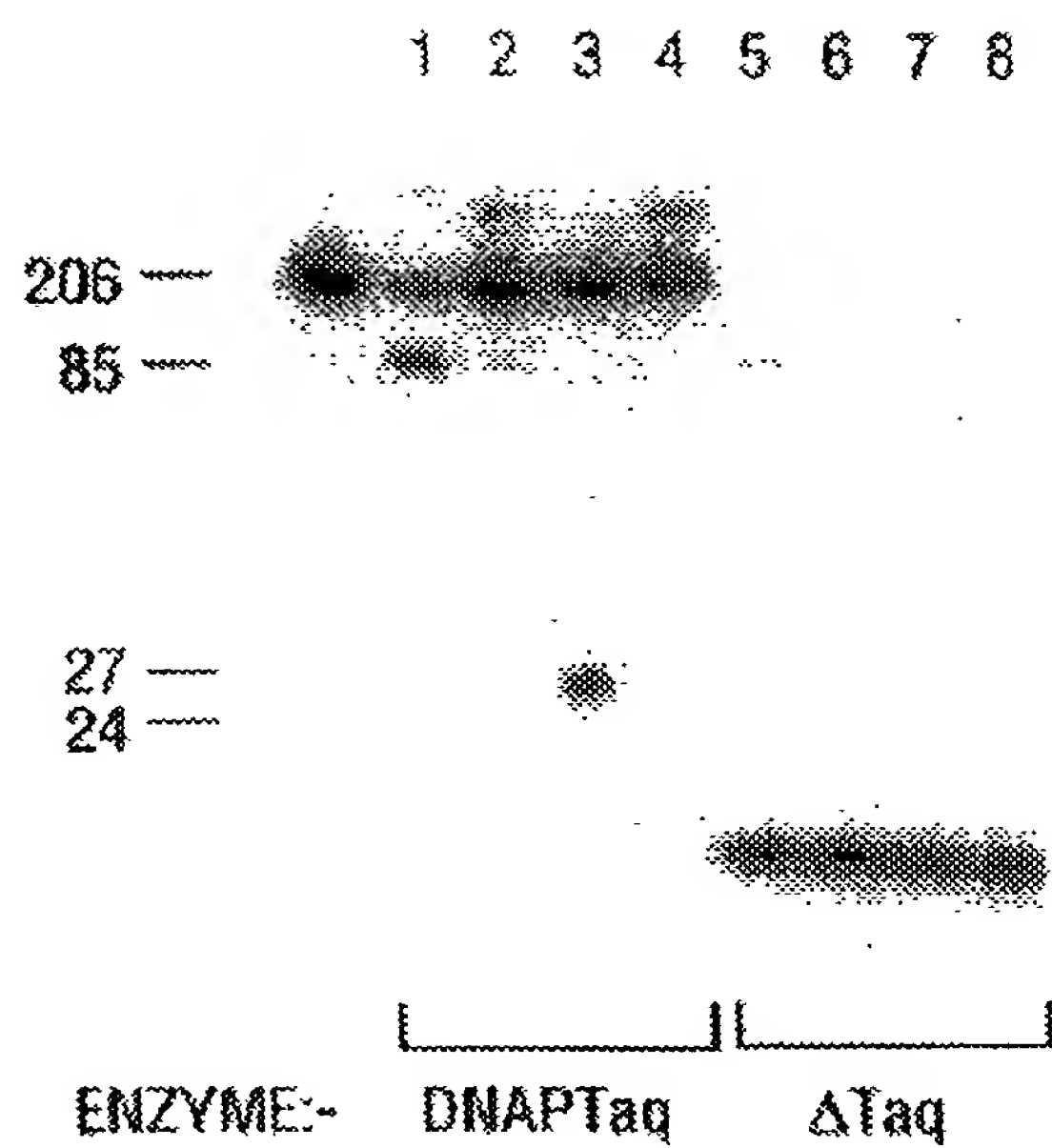


FIG. 25A

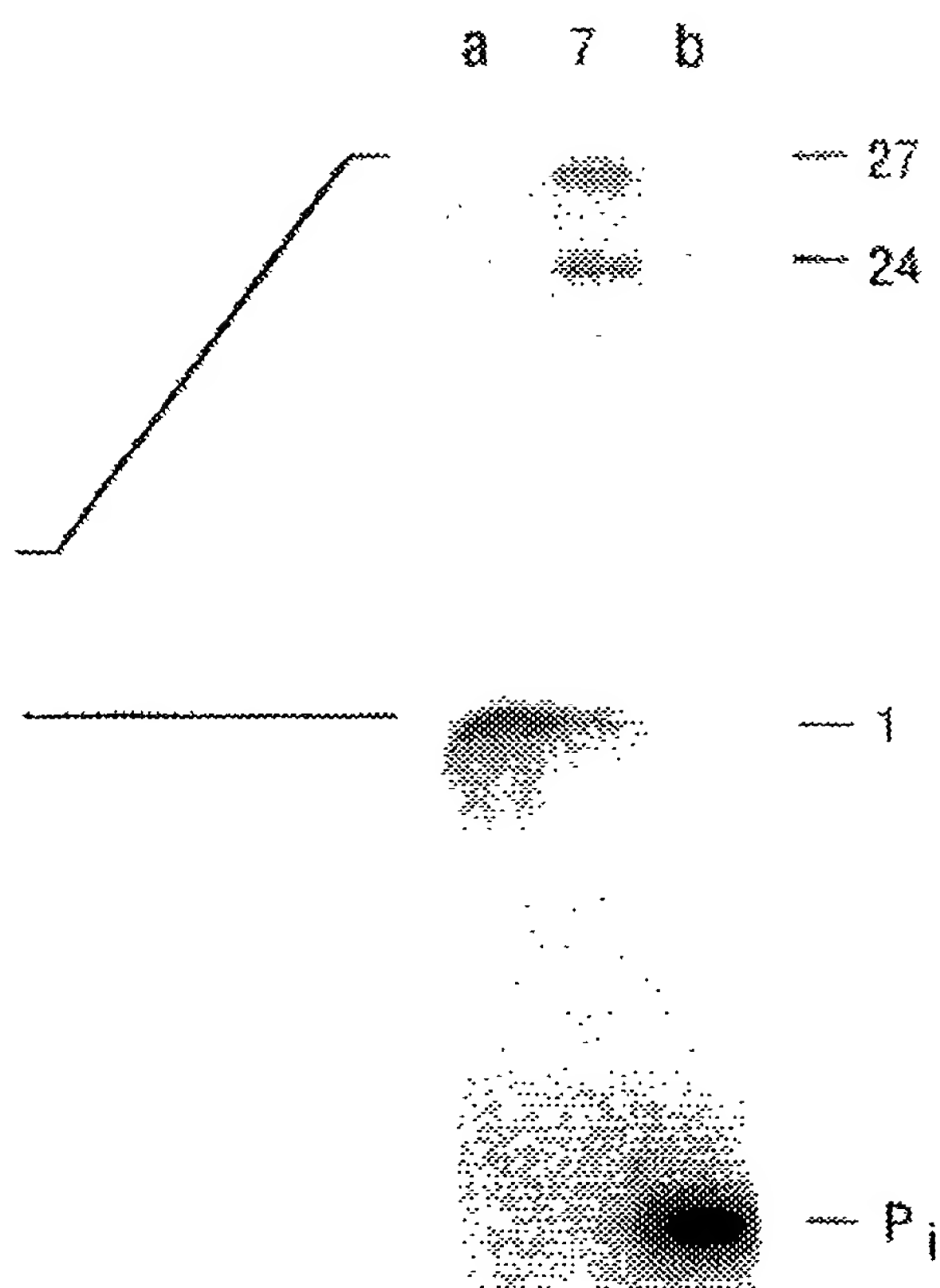


FIG. 25B

FIG. 26A

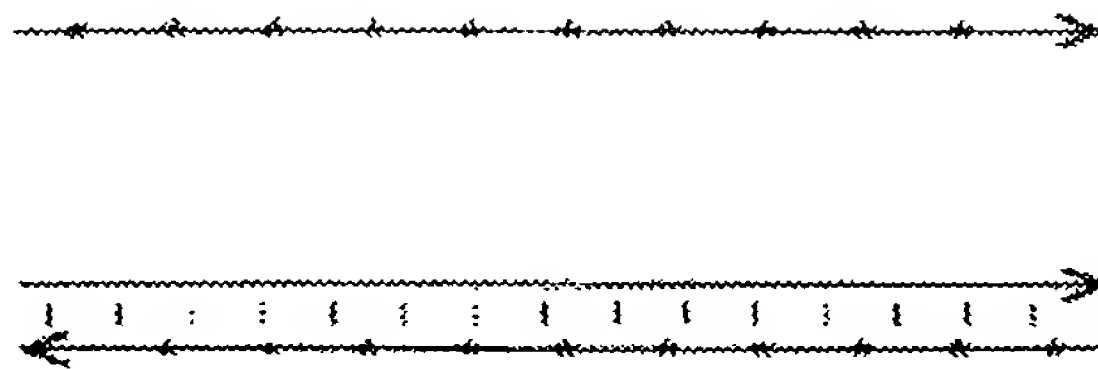
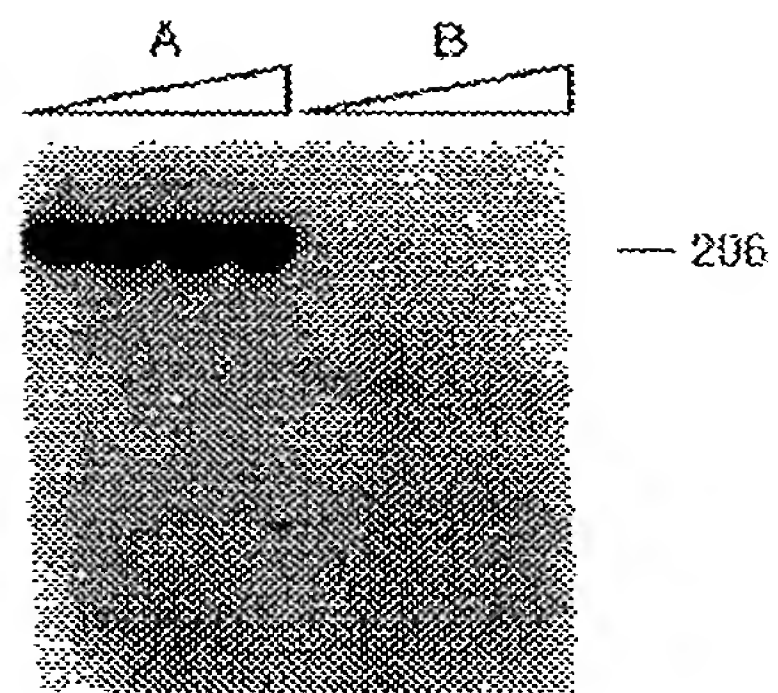


FIG. 26B

* = $3\lambda p$



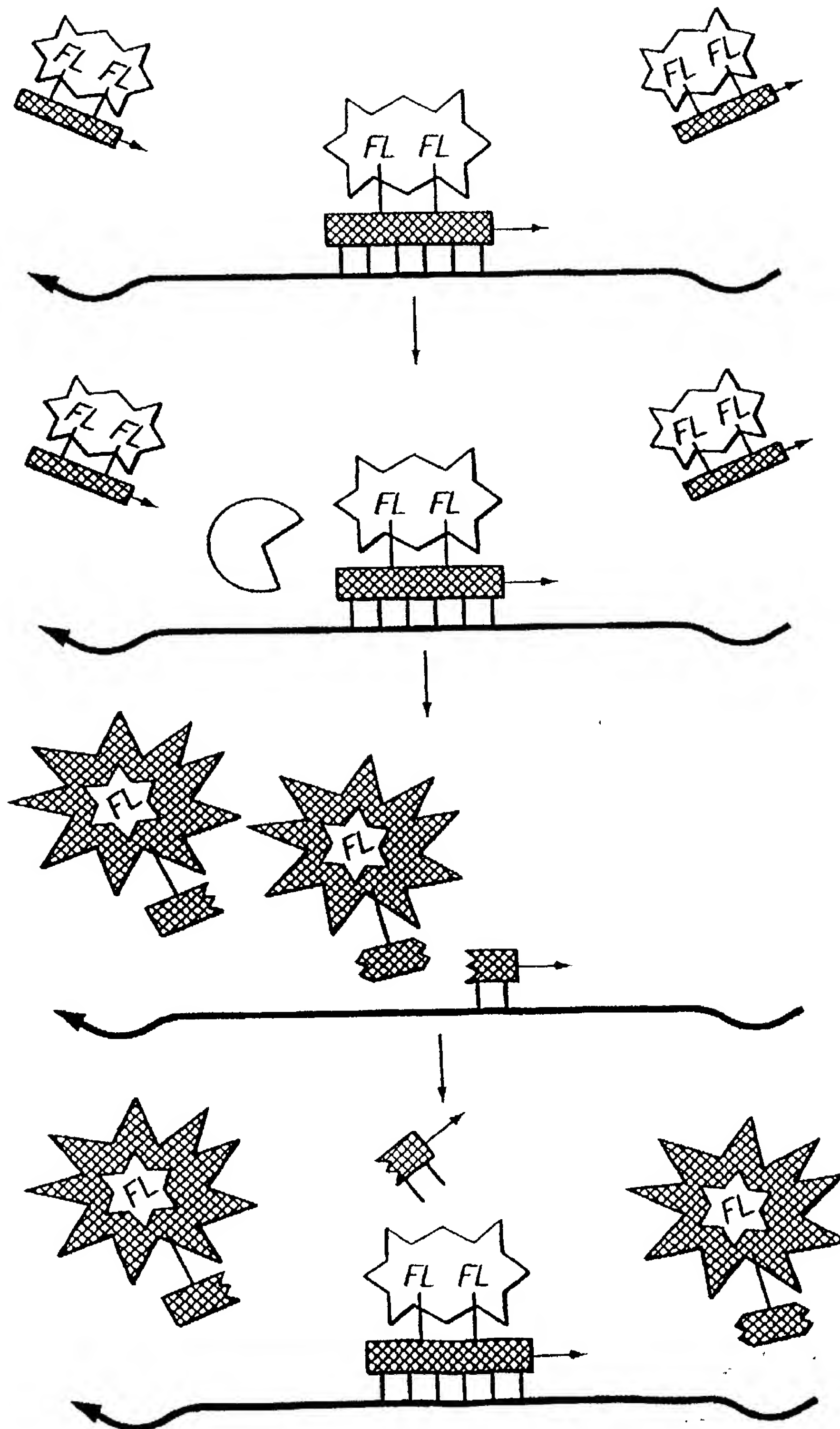
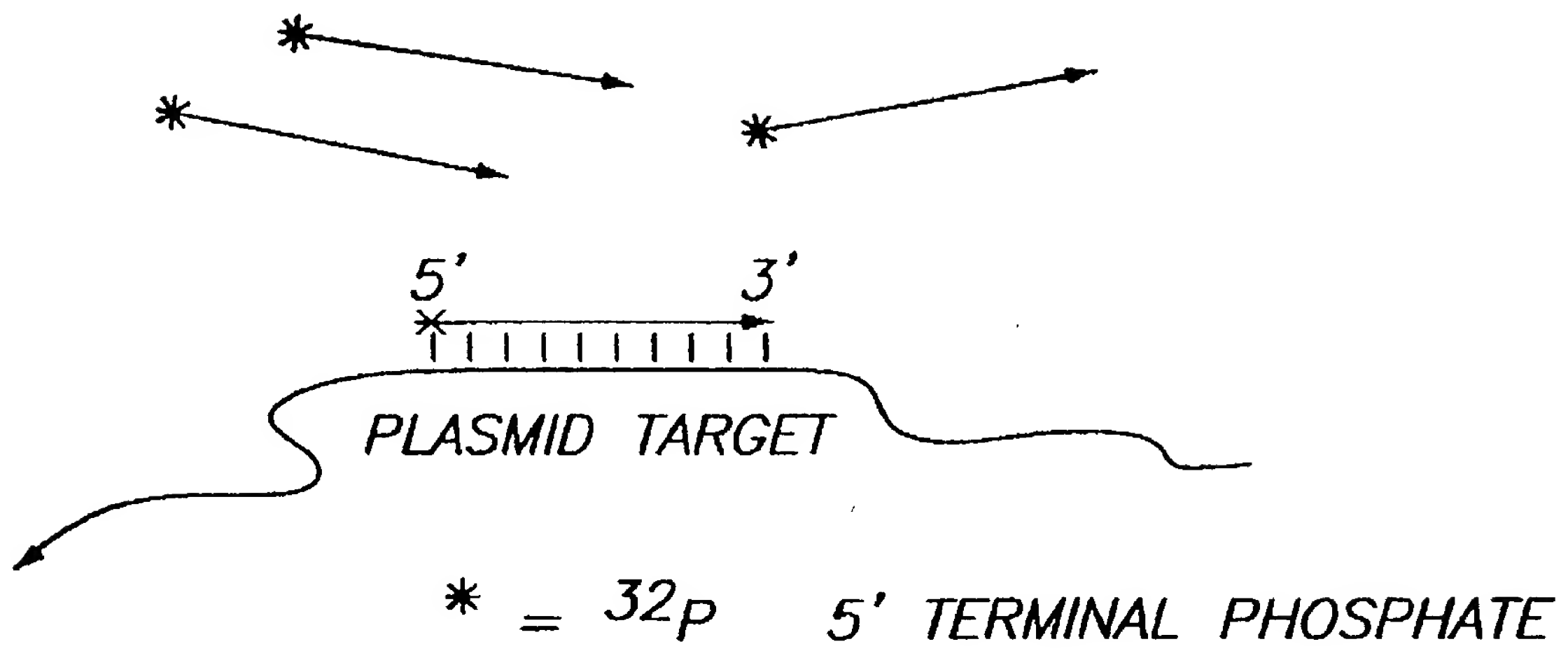
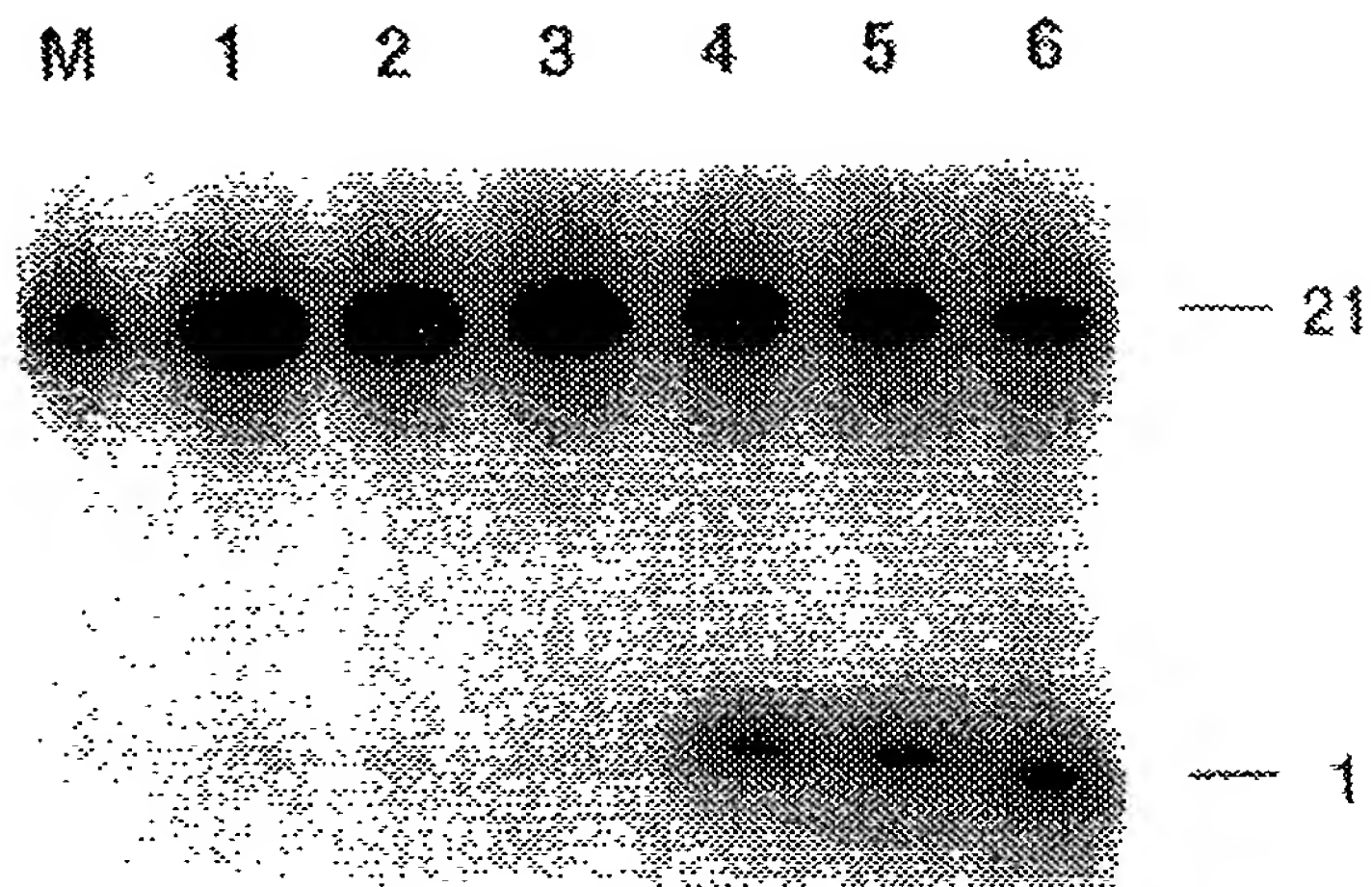


FIG. 27

**FIG. 28A**

**FIG. 28B**

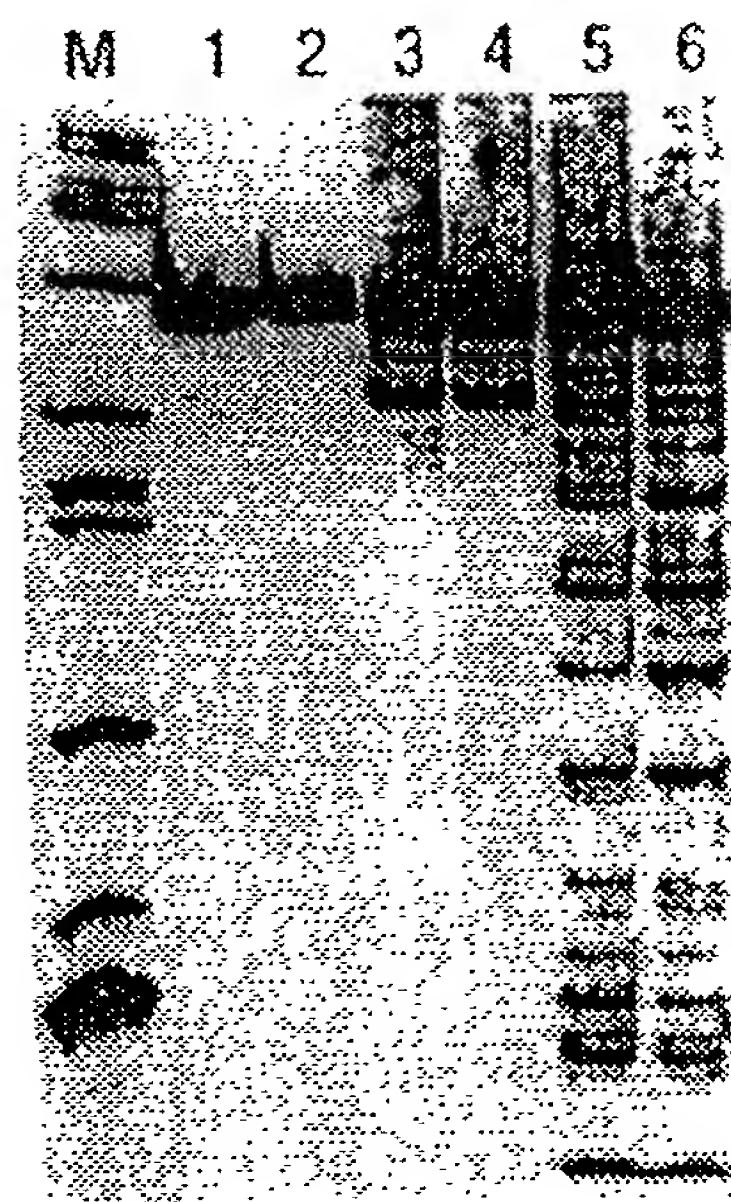


FIG. 30

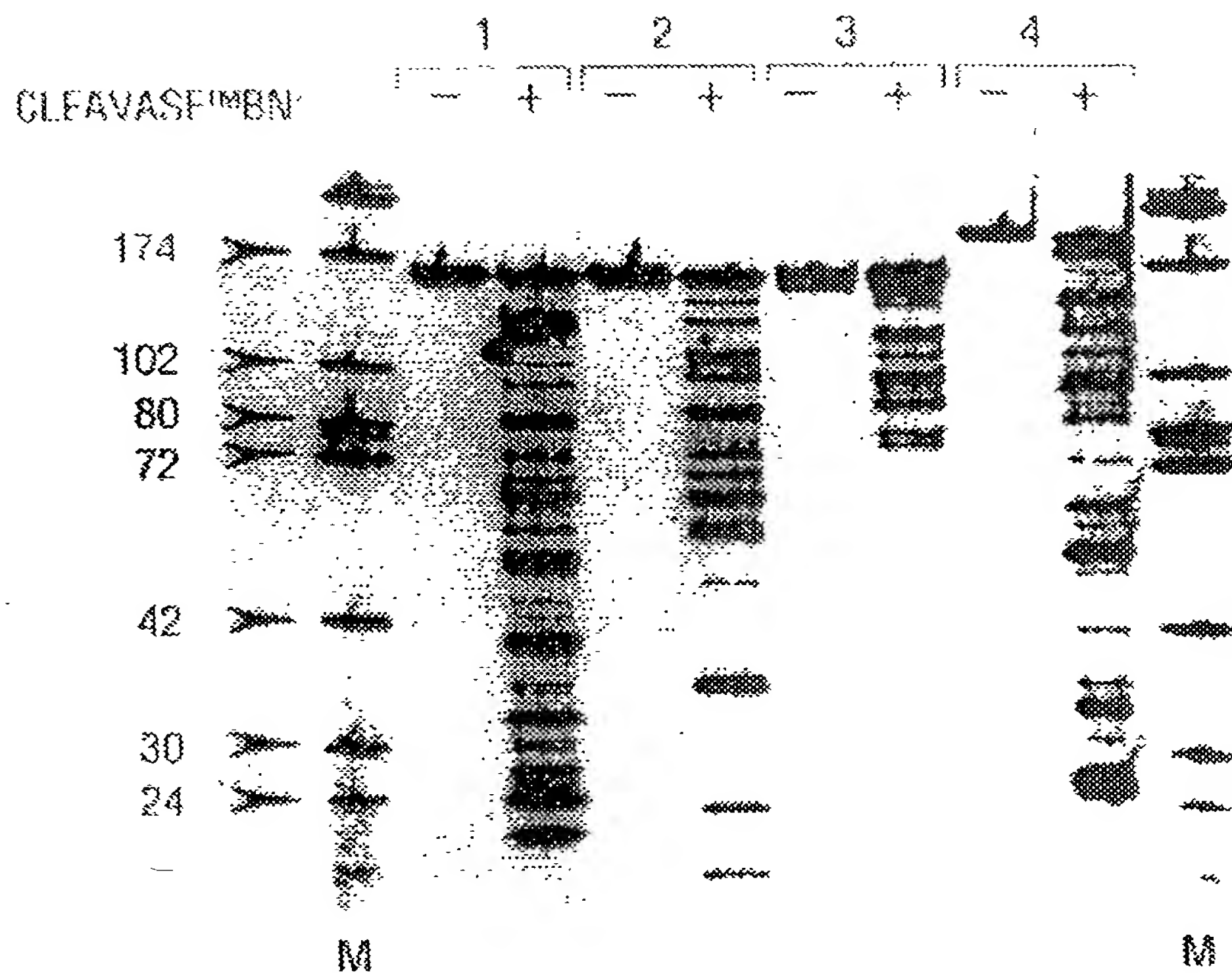


FIG. 31

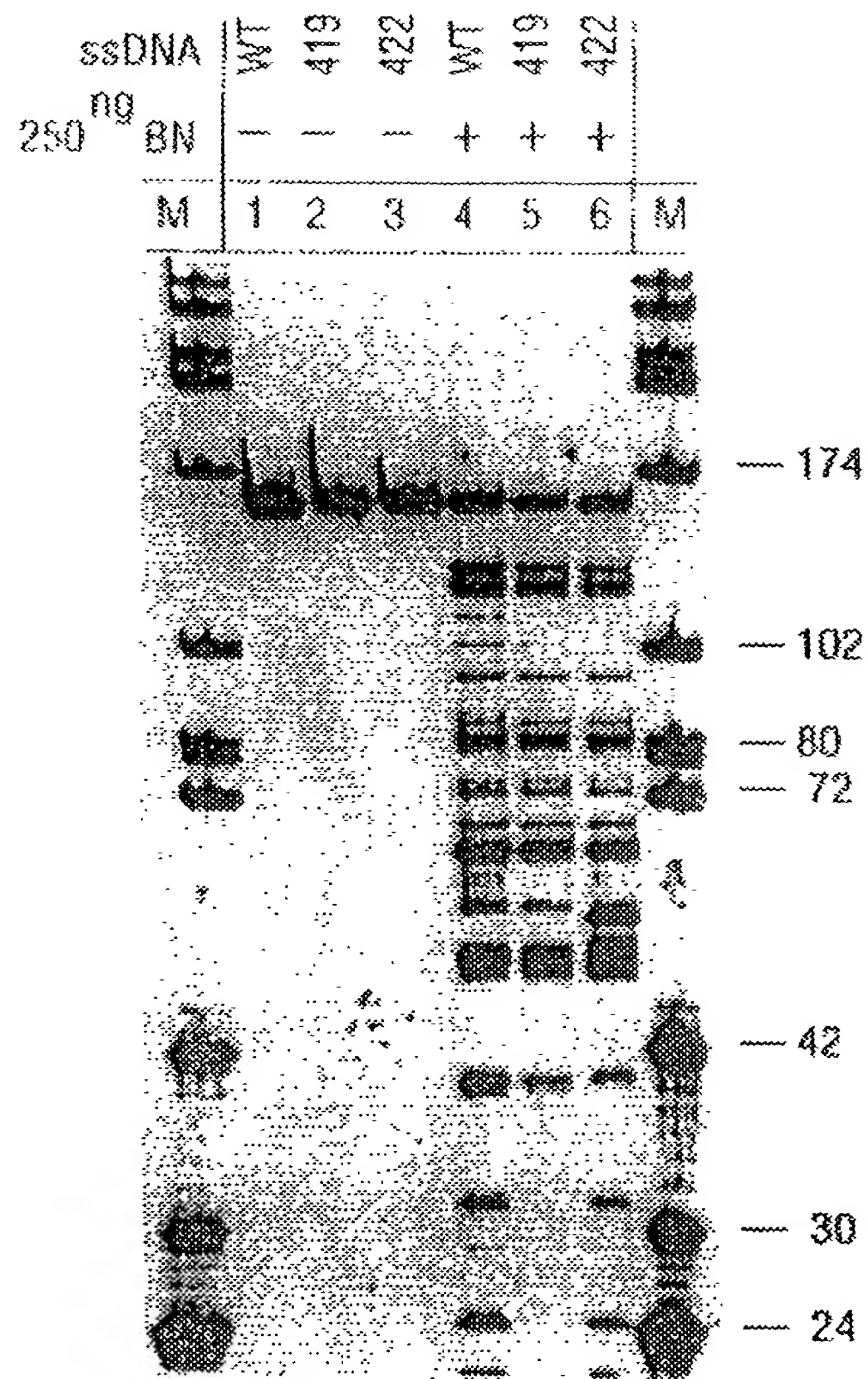
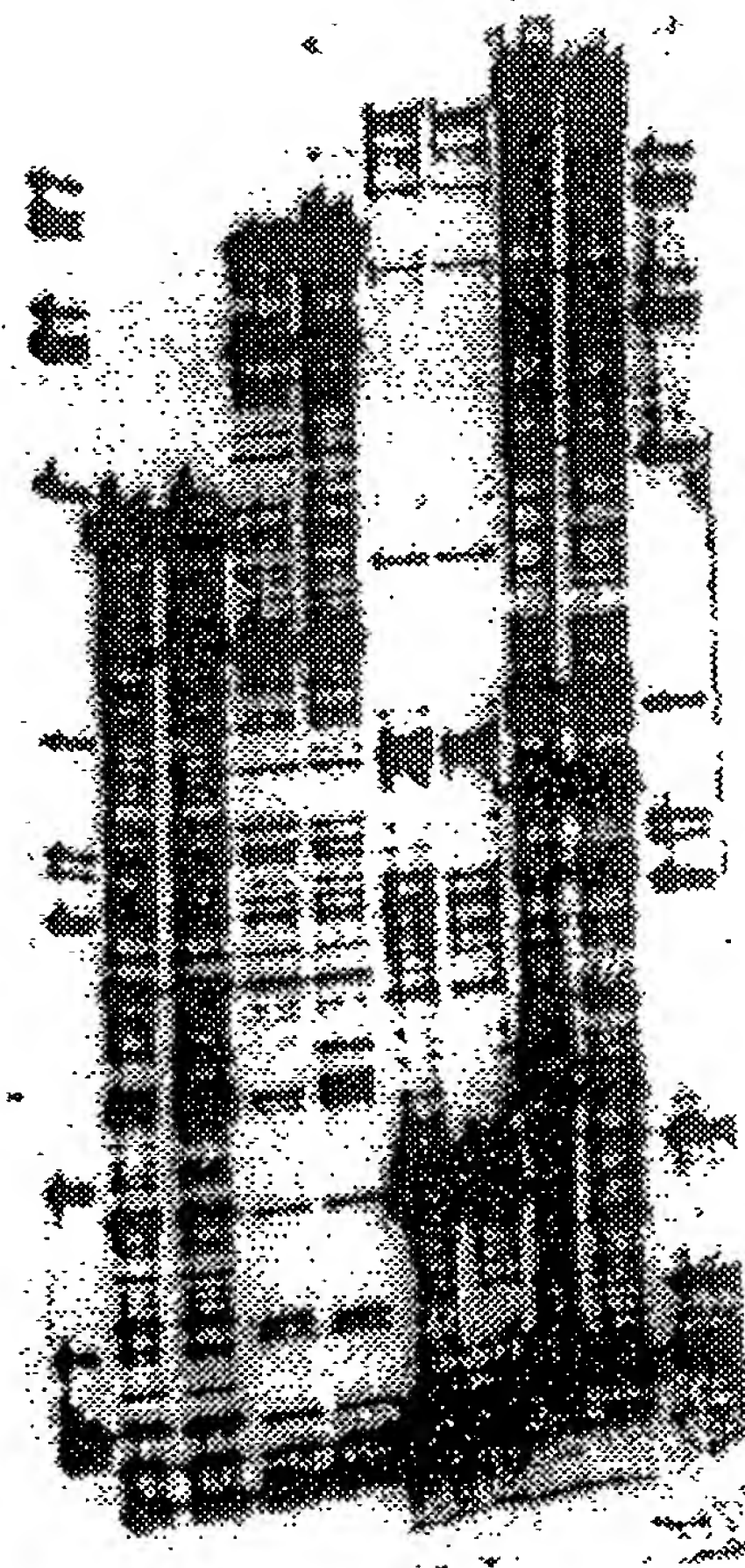


FIG. 32

157 378 1056 1587
M 1 2 3 4 5 6 7 8 M



WT 422 WT 422 WT 422 WT 422

FIG. 33



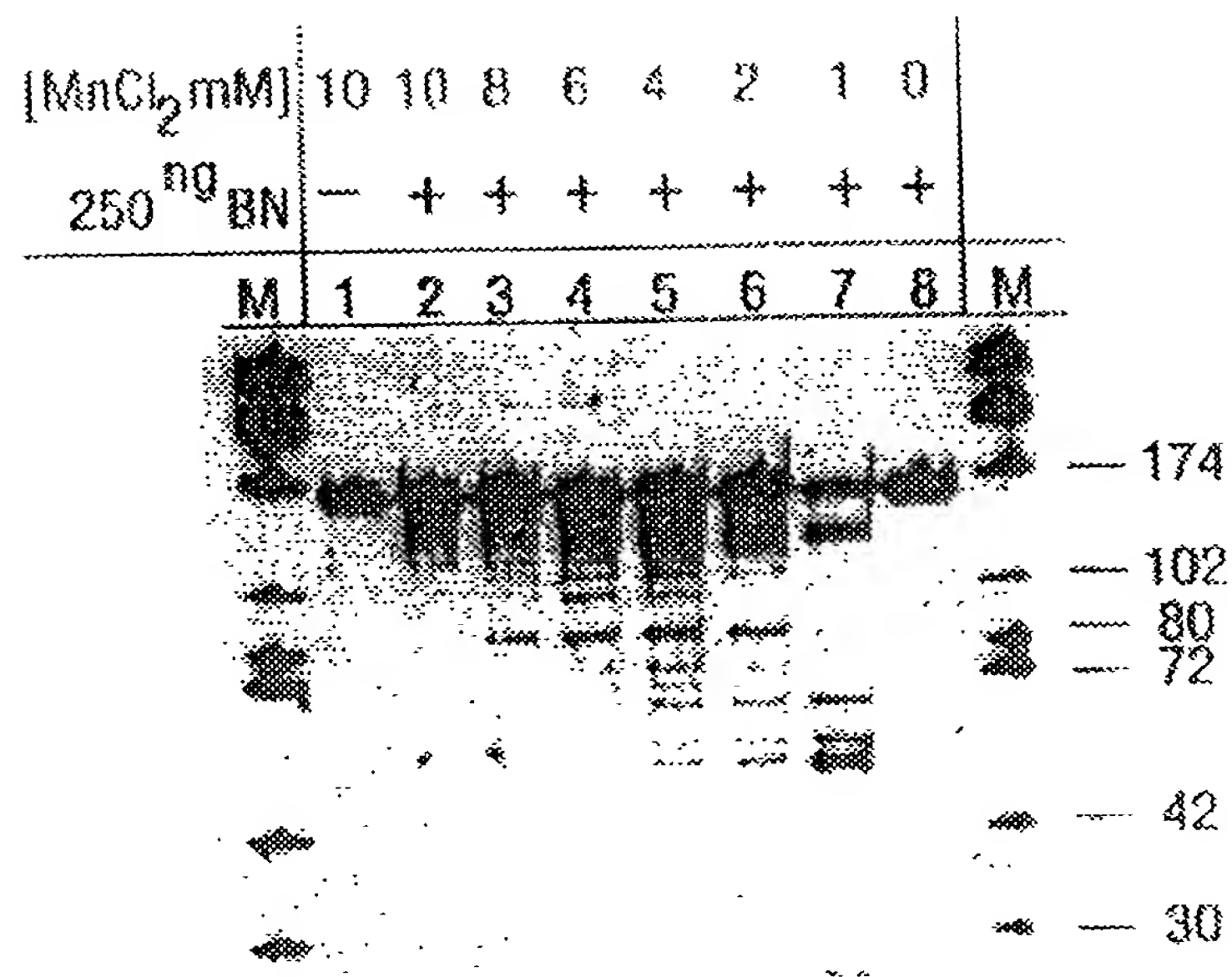


FIG. 34

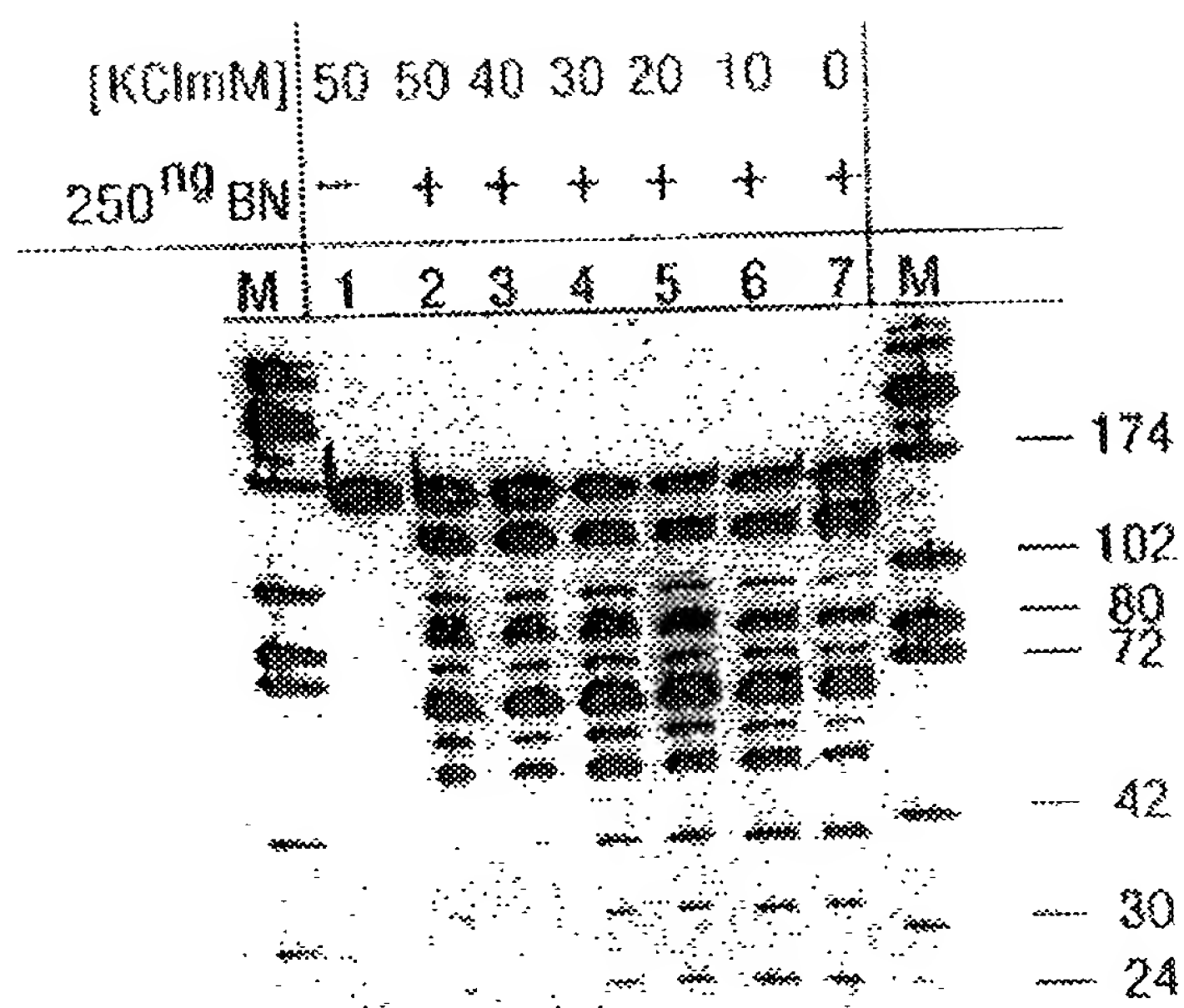


FIG. 35

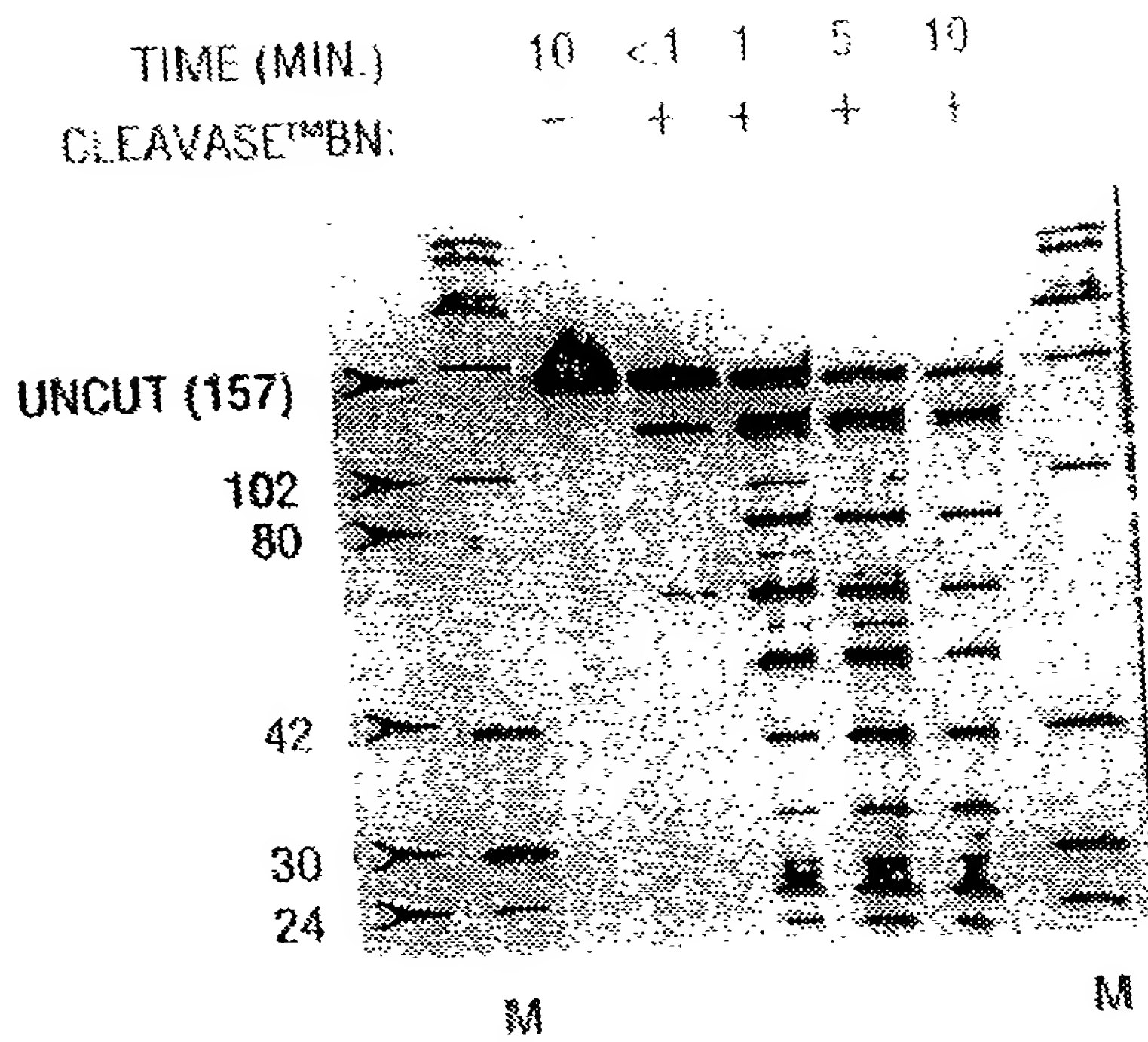


FIG. 36

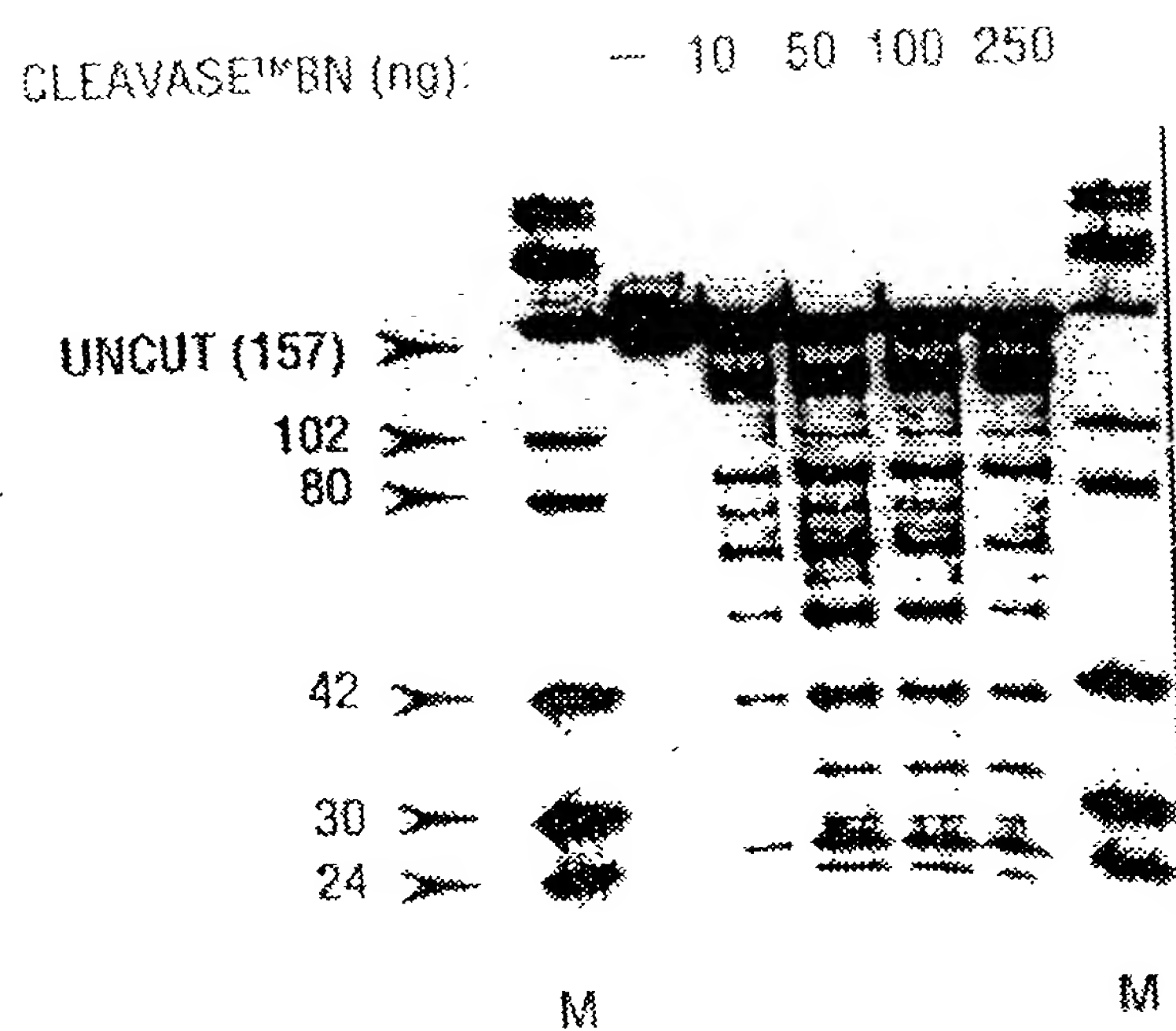


FIG. 38

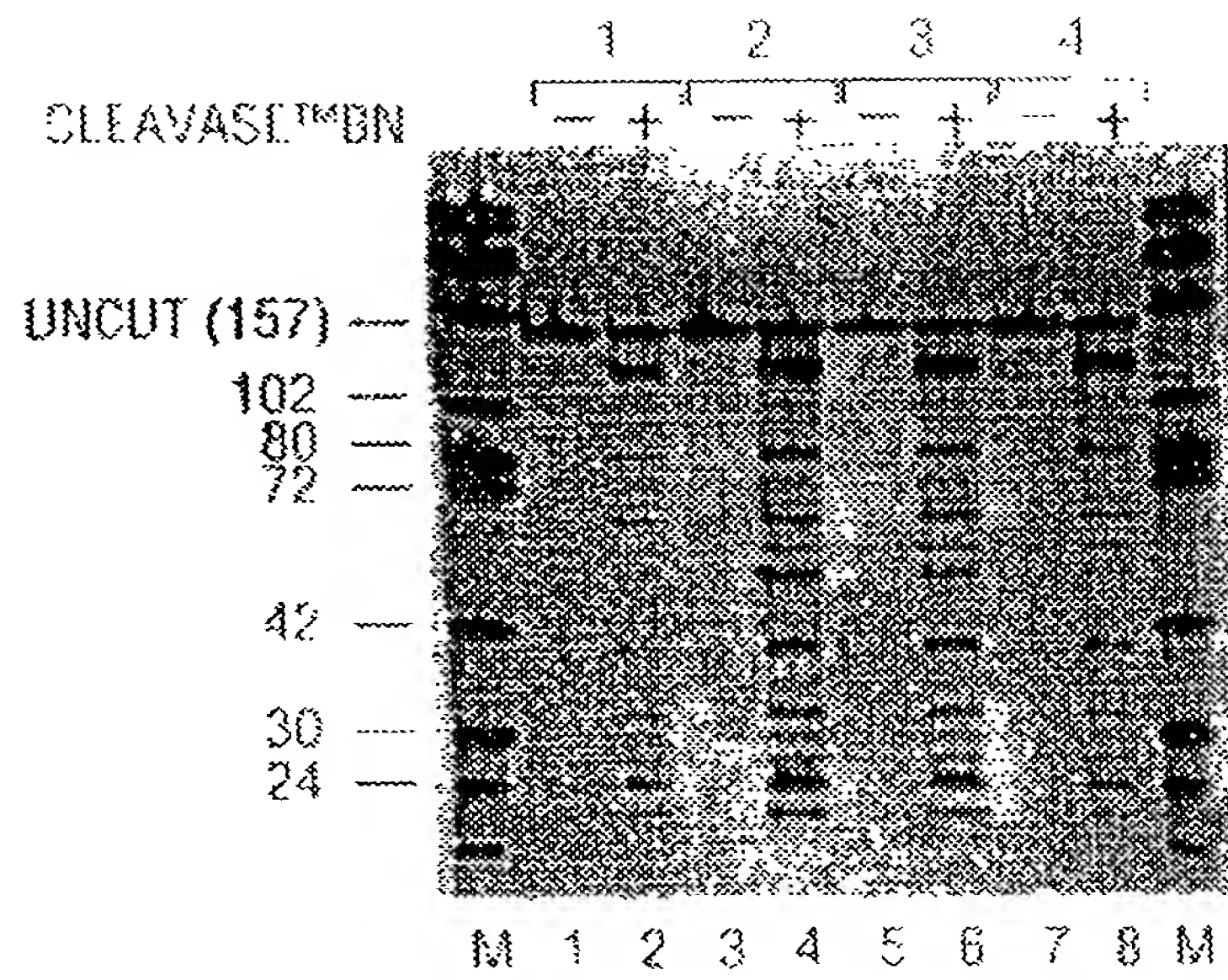


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ^{ng} BN	—	—	—	+	+	+	+	+	+	—	—	—
M	1	2	3	4	5	6	7	8	9	10	11	12

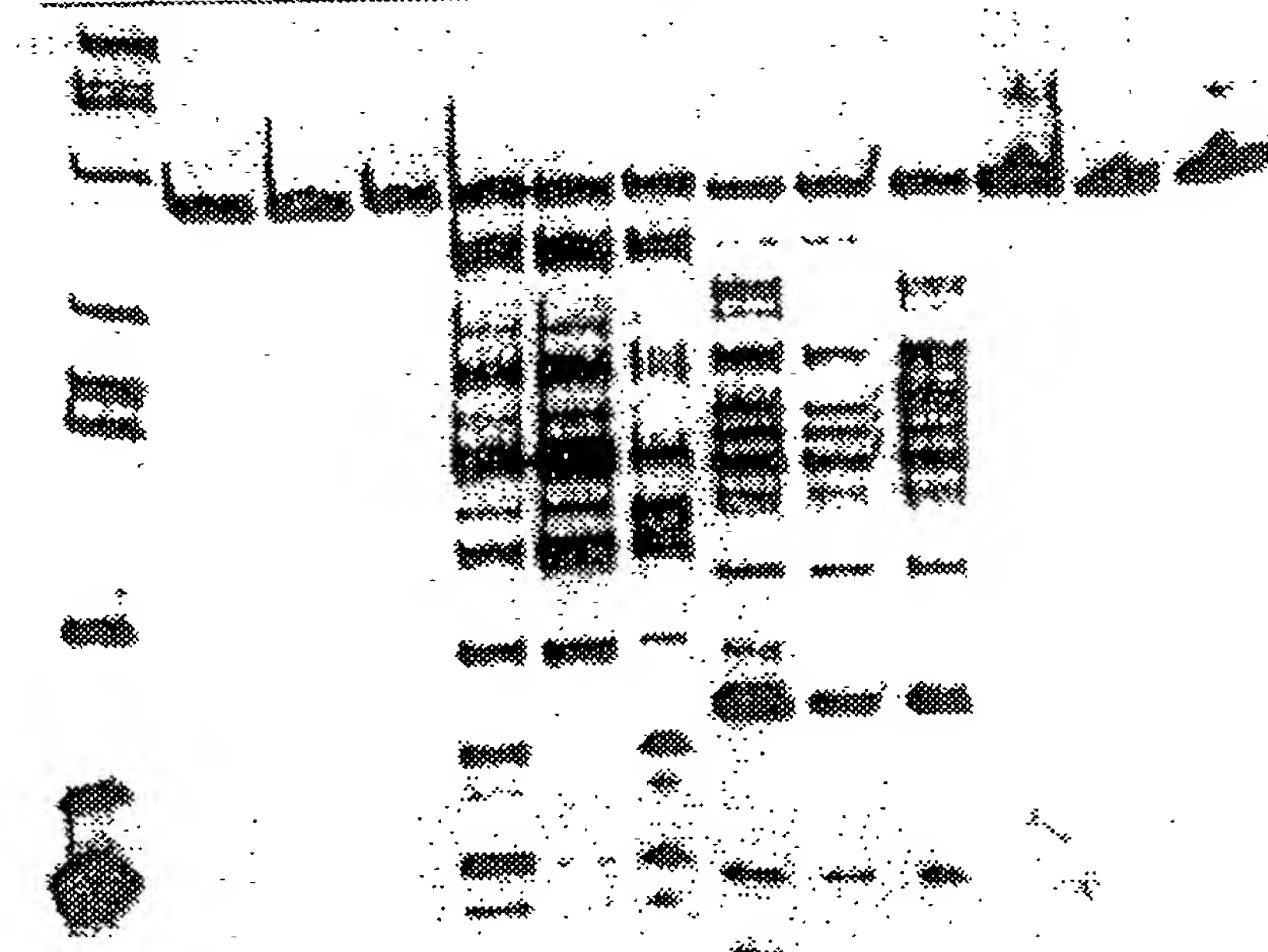


FIG. 40

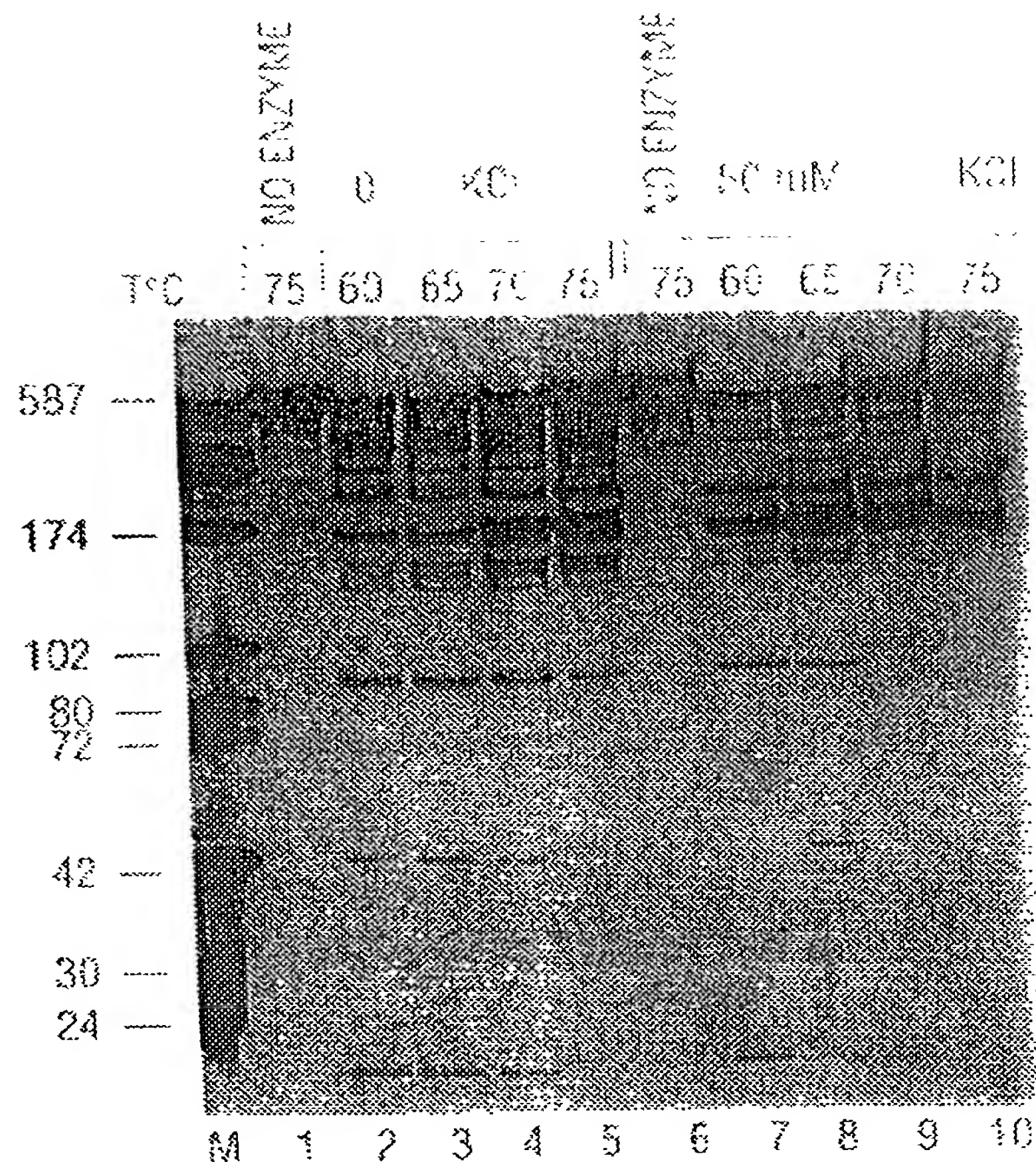


FIG. 41

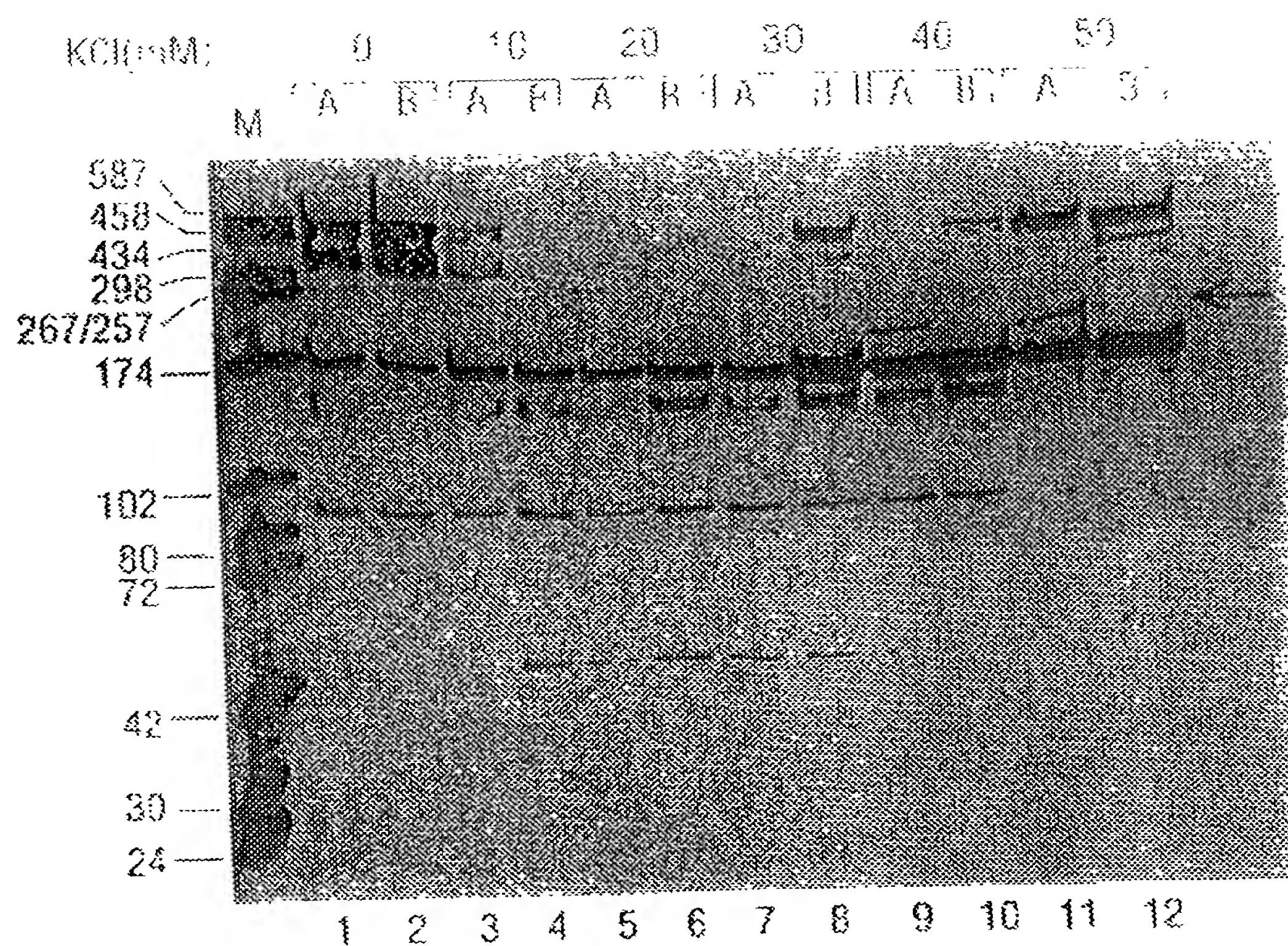


FIG. 42

CLEAVASE™BN

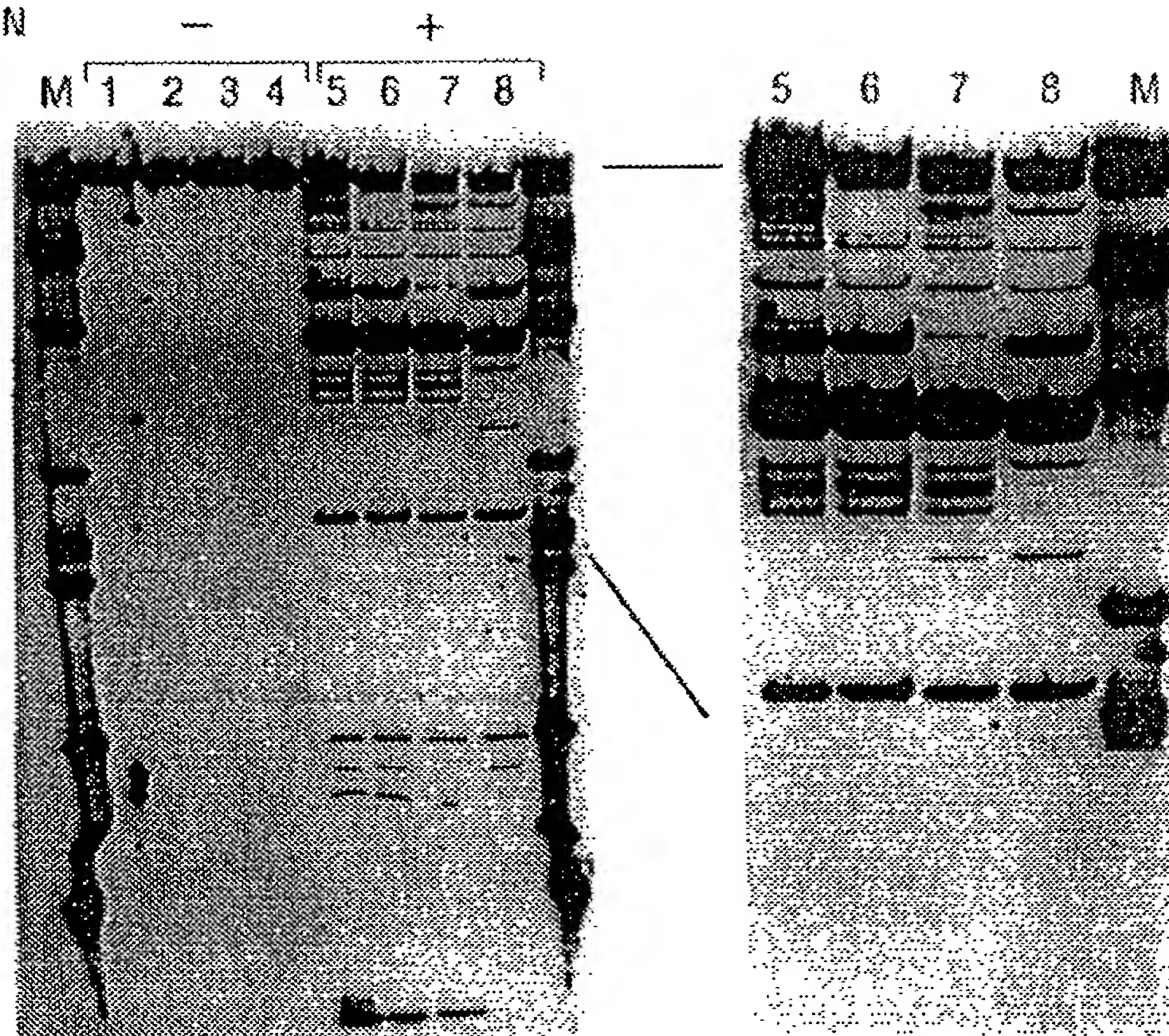


FIG. 43

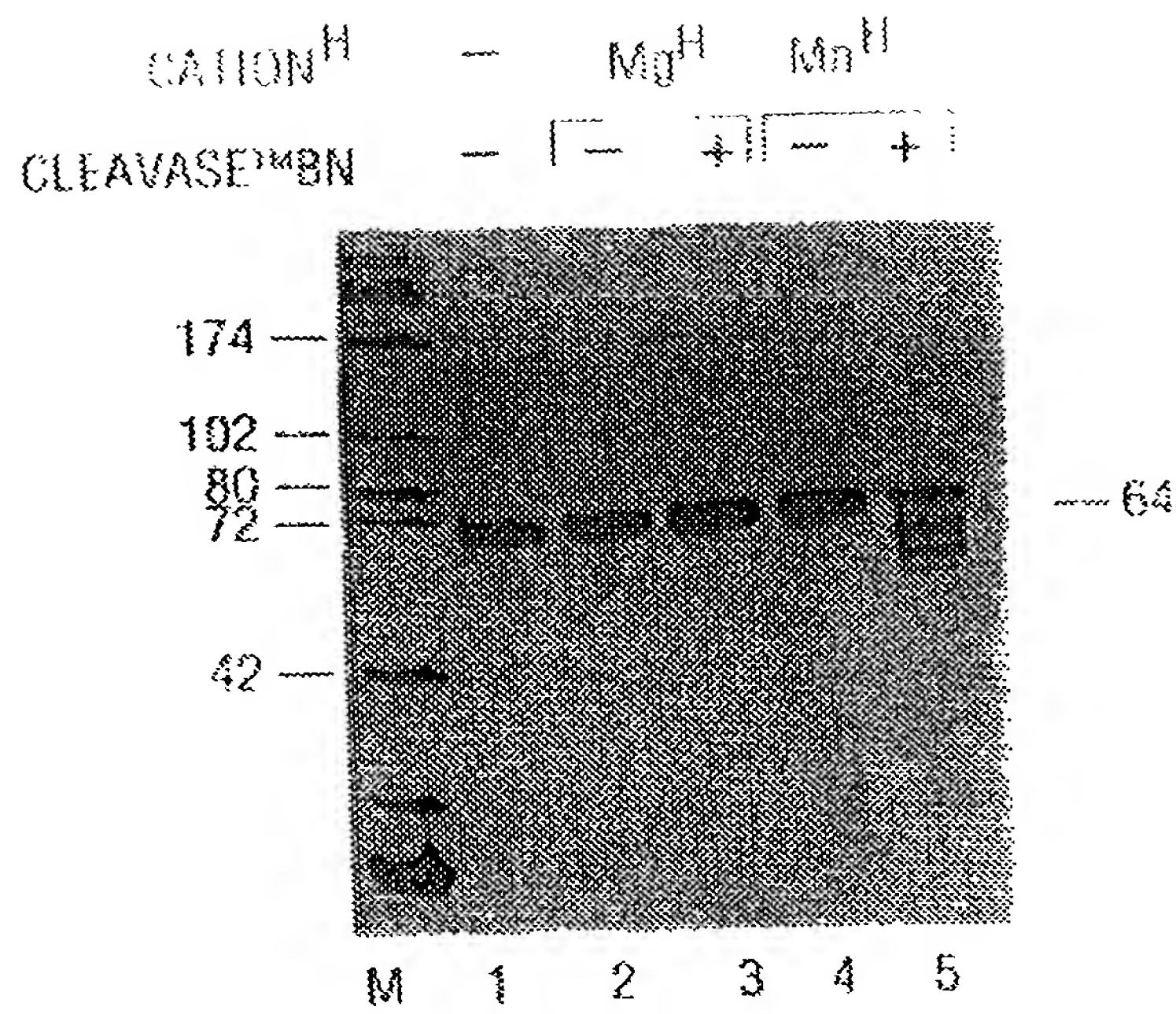


FIG. 44

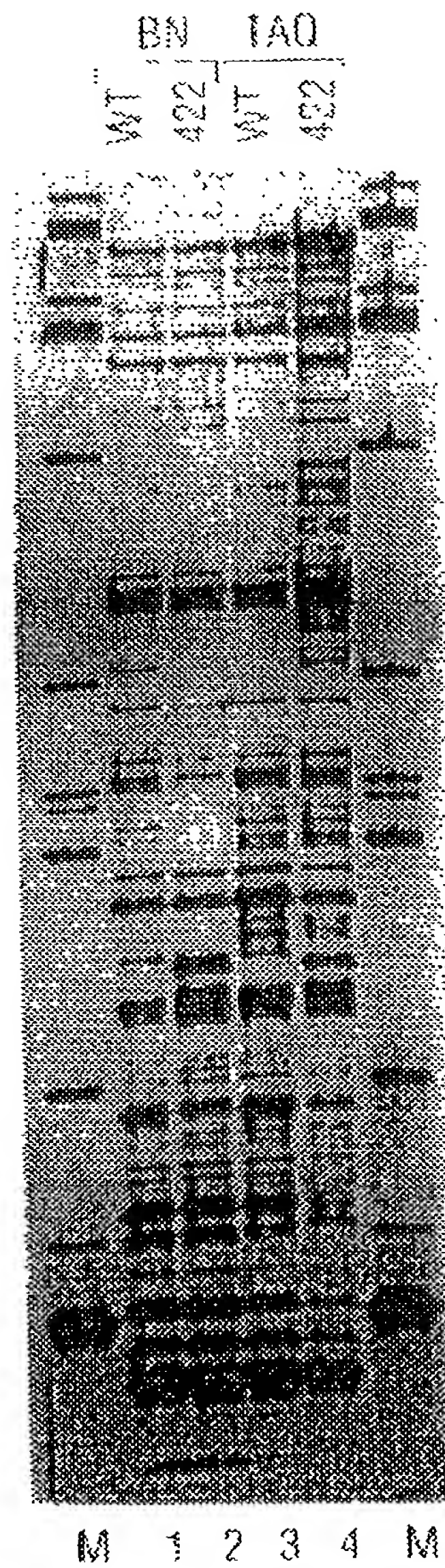


FIG. 45

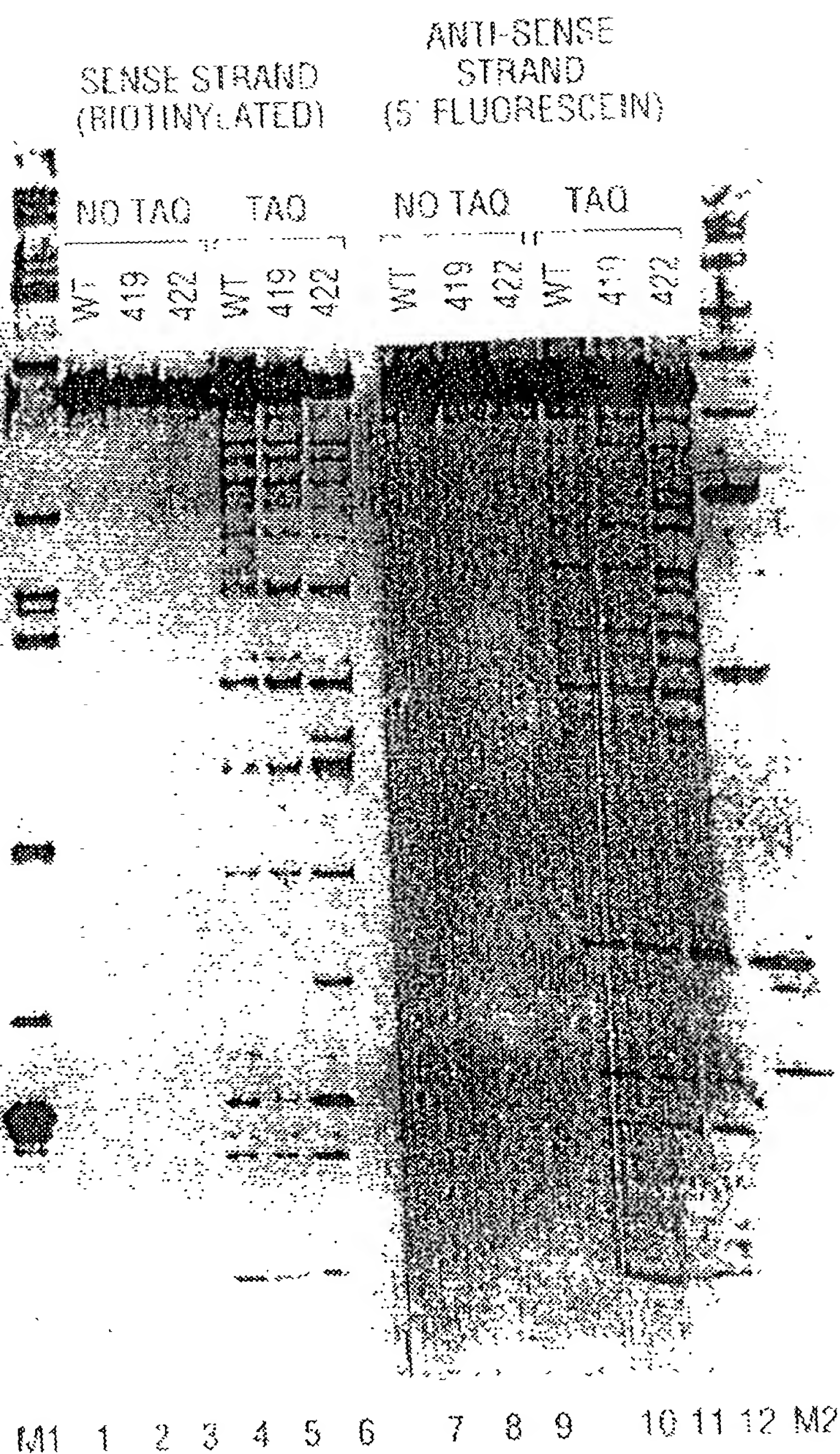


FIG. 46

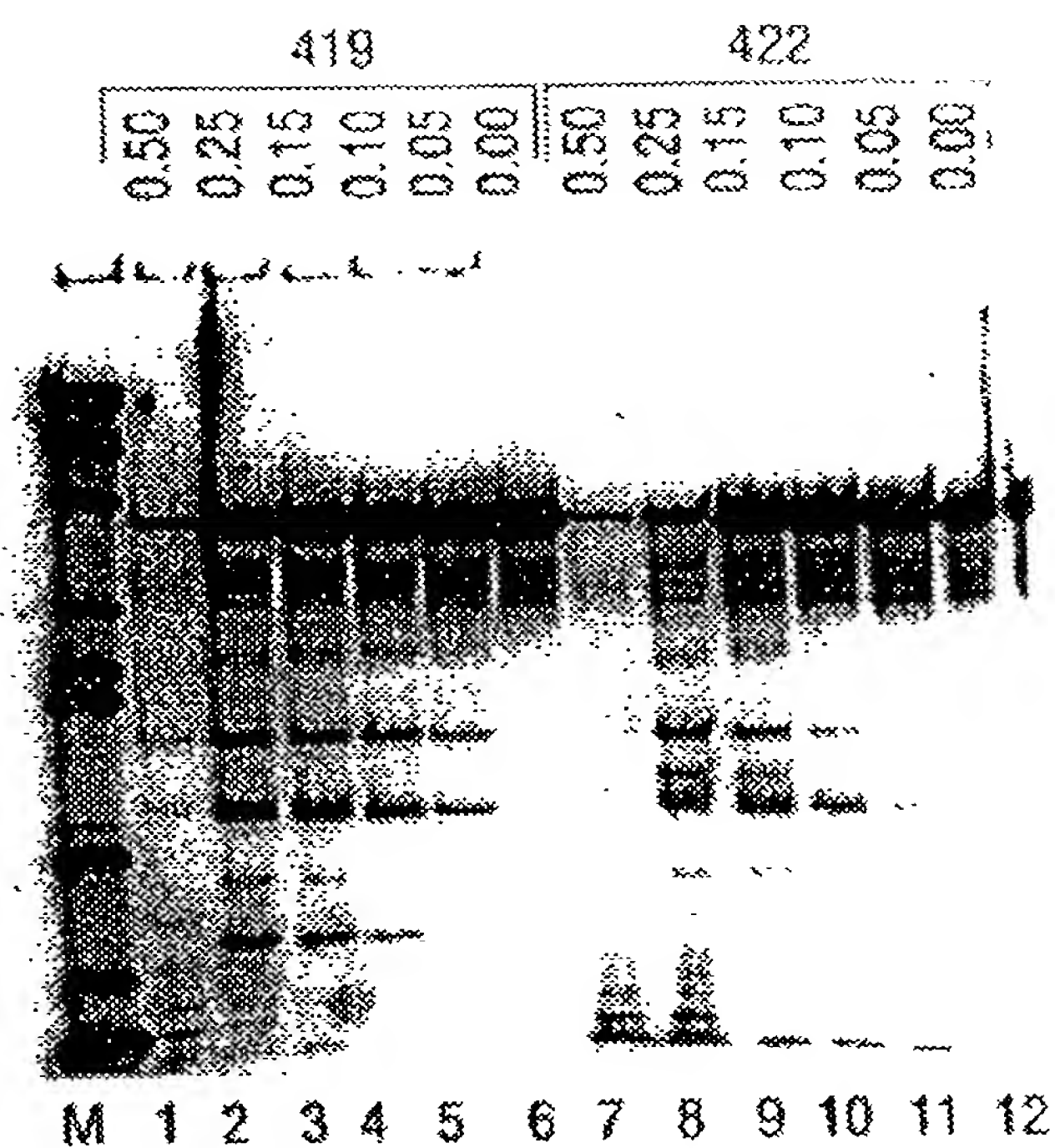


FIG. 47

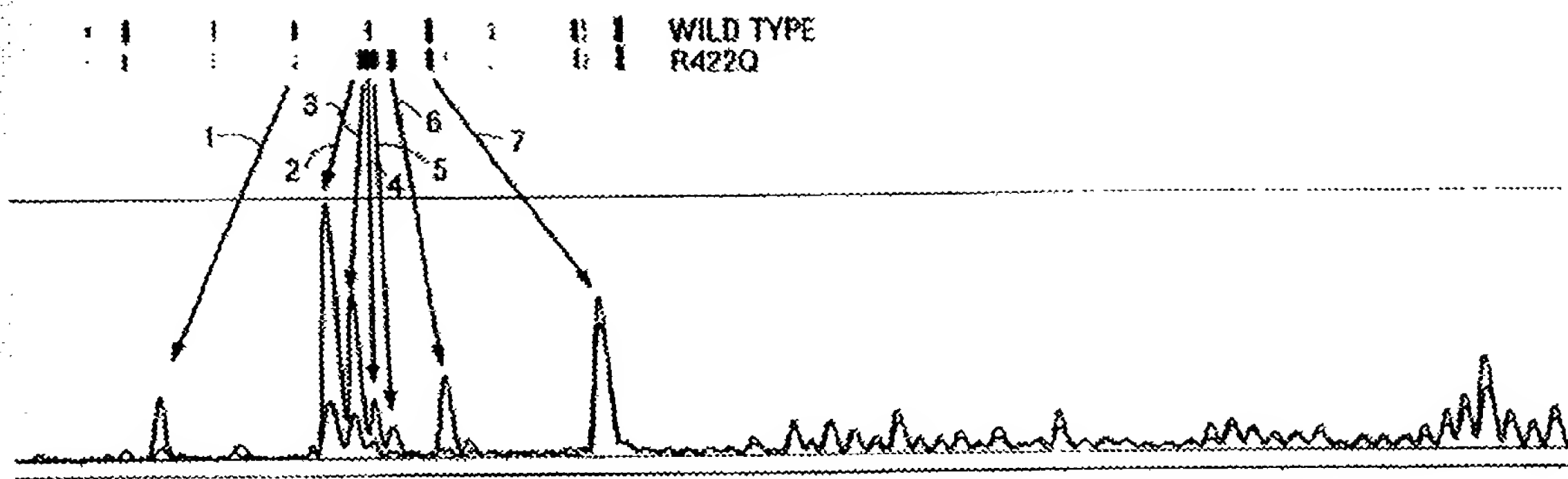


FIG. 48

L.100.8-1
(SEQ ID NO: 76) 5' GGCTGACAAGGAAGAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3' CCGACTGTTCTTCCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.46.16-10
(SEQ ID NO: 77) 5' GGCTGACAAGGAAGGAAGAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
3' CCGACTGTTCTTCCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12
(SEQ ID NO: 78) 5' GGCTGACAAGGAAGGAAGAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
3' CCGACTGTTCTTCCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3
(SEQ ID NO: 79) 5' GGCTGACAAGGAAGGAAGAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3' CCGACTGTTCTTCCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.CEM/251
(SEQ ID NO: 80) 5' GGCTGACAAGGAAGGAAGAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG
3' CCGACTGTTCTTCCCTTTGAGCGACTTTGTCGTCCCTGAAAGGTGTTCCCC

L.36.8-3
(SEQ ID NO: 81) 5' GGCTGACAAGGAAGGAAGAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3' CCGACTGTTCTTCCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A

09040925.022602

L.100.8-1 (SEQ ID NO: 76) 100
ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA
L.46.16-10 (SEQ ID NO: 77)
ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCACTTTCT
TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA
L.46.16-12 (SEQ ID NO: 78)
ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCACTTTCT
TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGGTGAAAGA
L19.16-3 (SEQ ID NO: 19)
ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGAGAGA
L.CEM/251 (SEQ ID NO: 80)
ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTCT
TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAAAGA
L.36.8-3 (SEQ ID NO: 81)
ATGTTACGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
TACAATGCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA

FIG. 49B

150

L.100.8-1	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.46.16-10	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.46.16-12	5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCCGGA 3'ACCACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.19.16-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.CEM/251	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT
L.36.8-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGGCTCTGCCGGA 3'ACTACATATTTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCCT

FIG. 49C

L.100.8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCTCCAAGAGAGGTCGTGATCGTCCATC	200
L.46.16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCTCCAAGAGAGGTCGTGATCGTCCATC	
L.46.16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCTCCAAGAGAGGTCGTGATCGTCCATC	
L.19.16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCTCCAAGAGAGGTCGTGATCGTCCATC	
L.CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCTCCAAGAGAGGTCGTGATCGTCCATC	
L.36.8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC	

FIG. 49D

09940925.022502

250

L. 100. 8 -1 5'AGCCTGGGTGTTCCCTGCTAGAC TCTCACCAGCAC TTGGCCGGTGCTGGG
(SEQ ID NO: 76) 3'TCGGACCCACAAGGGACCATCTGAGAGTGGTCGTGAACCGGCCACGACCC

L. 46.16-10 5'AGCCTGGGTGTTCCCTGCTAGAC TCTCACCAGCAC TTAGCCAGTGCTGGG
(SEQ ID NO: 77) 3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAATCGGTCACGACCC

L. 46.16-12 5'AGCCTGGGTGTTCCCTGCTAGAC TCTCACCAGCAC TTGGCCAGTGCTGGG
(SEQ ID NO: 78) 3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAACCGGTCACGACCC

L. 19.16-3 5'AGCCTGGGTGTTCCCTGCTAGAC TCTCACCAGCAC TTGGCCGGTGCTGGG
(SEQ ID NO: 79) 3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC

L. CEM/251 5'AGCCTGGGTGTTCCCTGCTAGAC TCTCACCAGCAC TTGGCCGGTGCTGGG
(SEQ ID NO: 80) 3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC

L. 36.8-3 5'AGCCTGAGTGTTCCCTGCTAAAC TCTCACCAGCAC TTGGCCGGTGCTGGG
(SEQ ID NO: 81) 3'TCGGACTCACAAAGGGACGATTTGAGAGTGGTCGTGAACCGGCCACGACCC

HAIRPIN

FIG. 49E

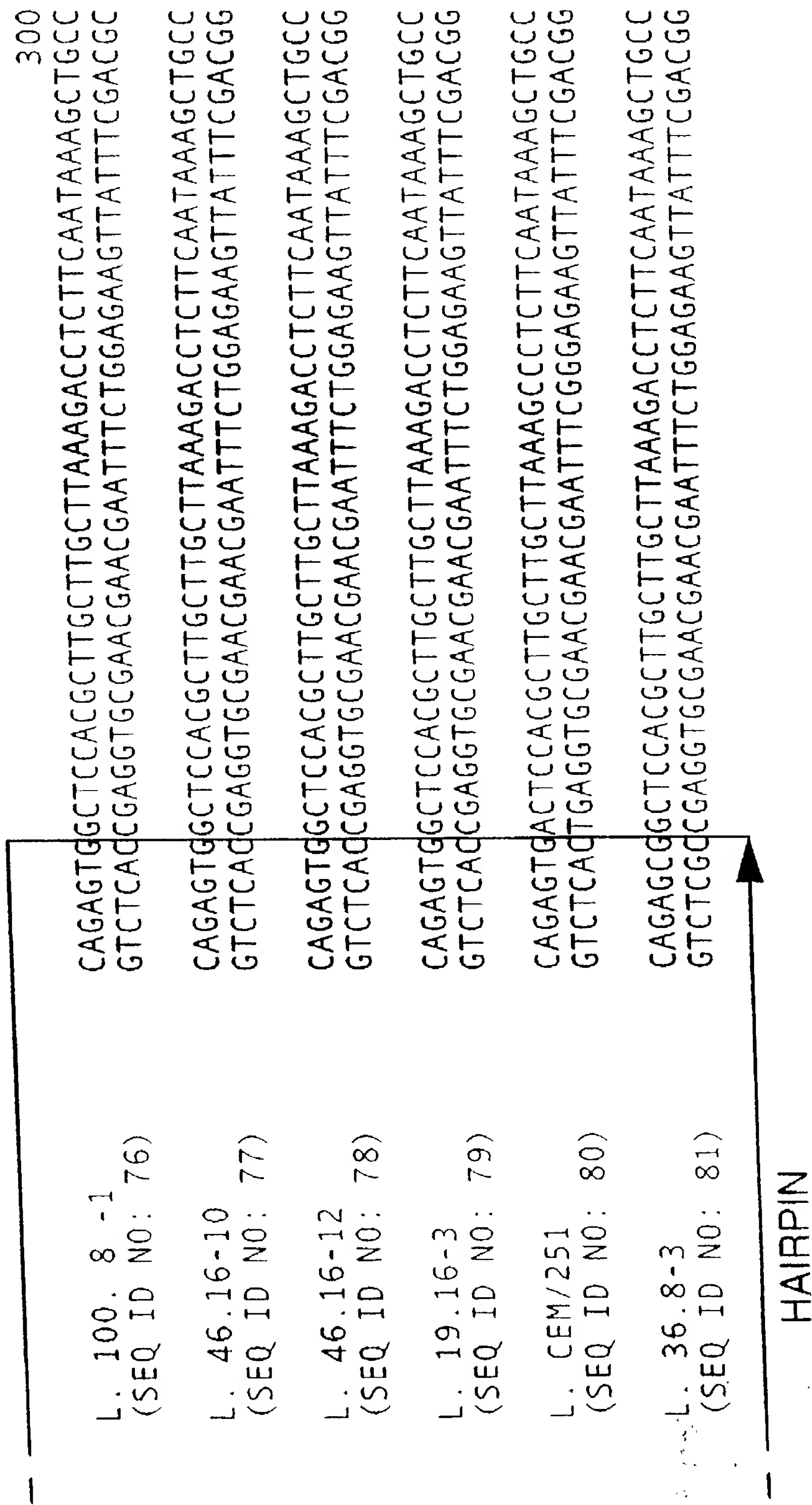


FIG. 49F

L. 100.8-1	<div>350</div> 5' ATTTT TAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATCCGGTCACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'
L. 46.16-10	5' ATTTT TAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATTCCGGTCACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'
L. 46.16-12	5' ATTTT TAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATTCCGGTCACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'
L. 19.16-3	5' ATTTT TAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'
L. CEM/251	5' ATTTT TAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATTCGATCACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'
L. 36.8-3	5' ATTTT TAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCCTG G 3' 3' TAAATCTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCGGGGAC C 5'

FIG. 49G

09940925 . 022602

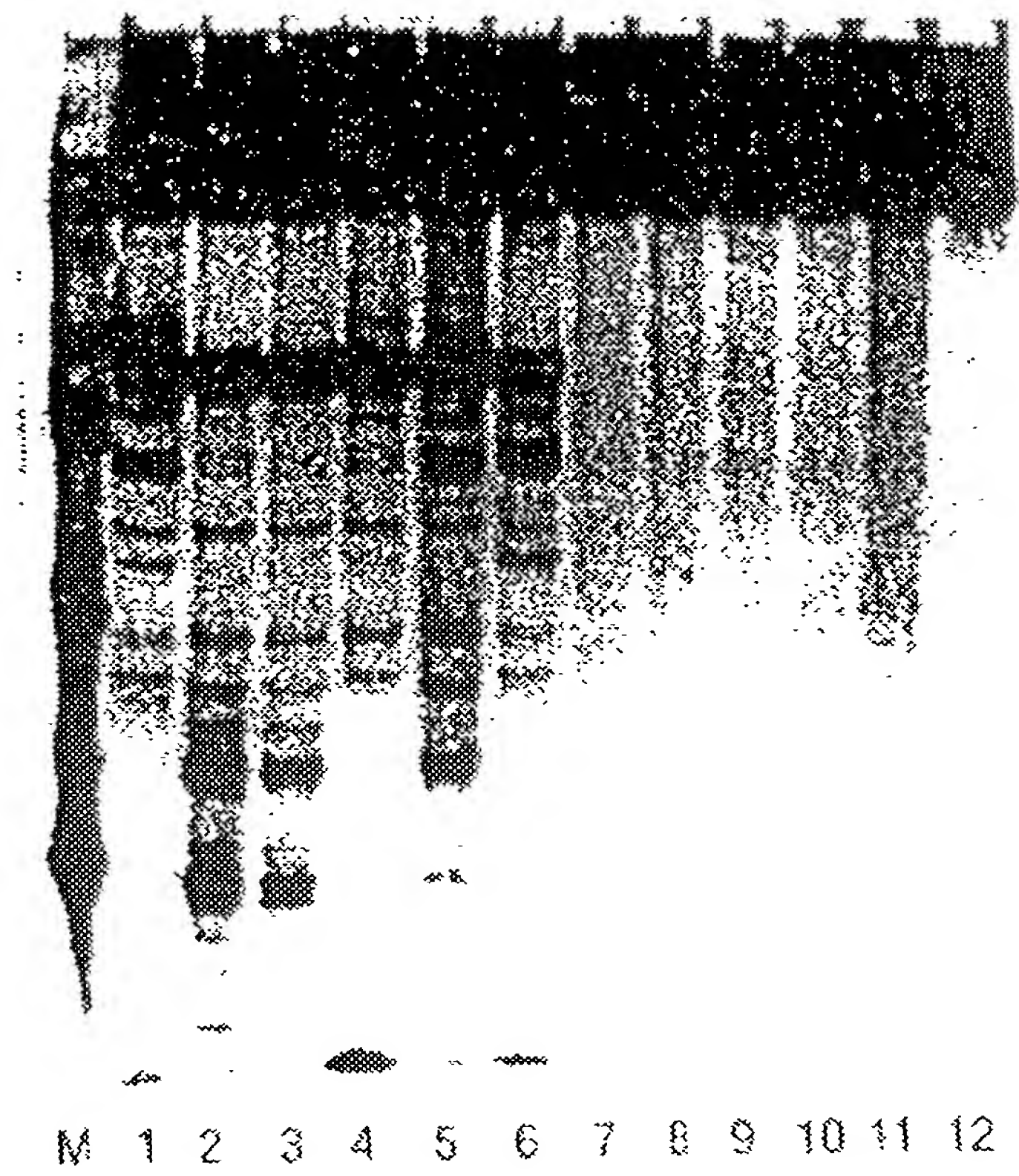


FIG. 50

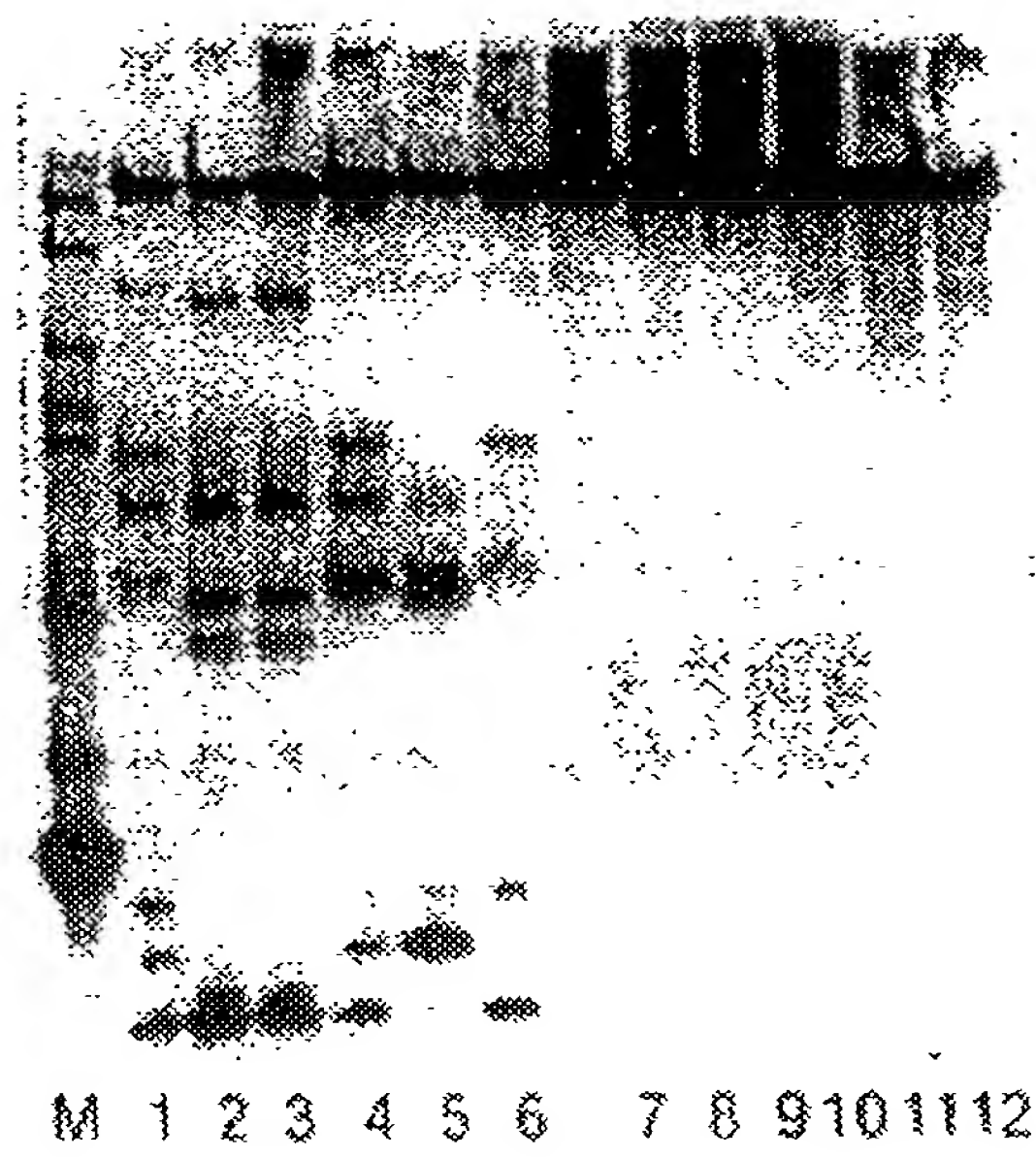


FIG. 51

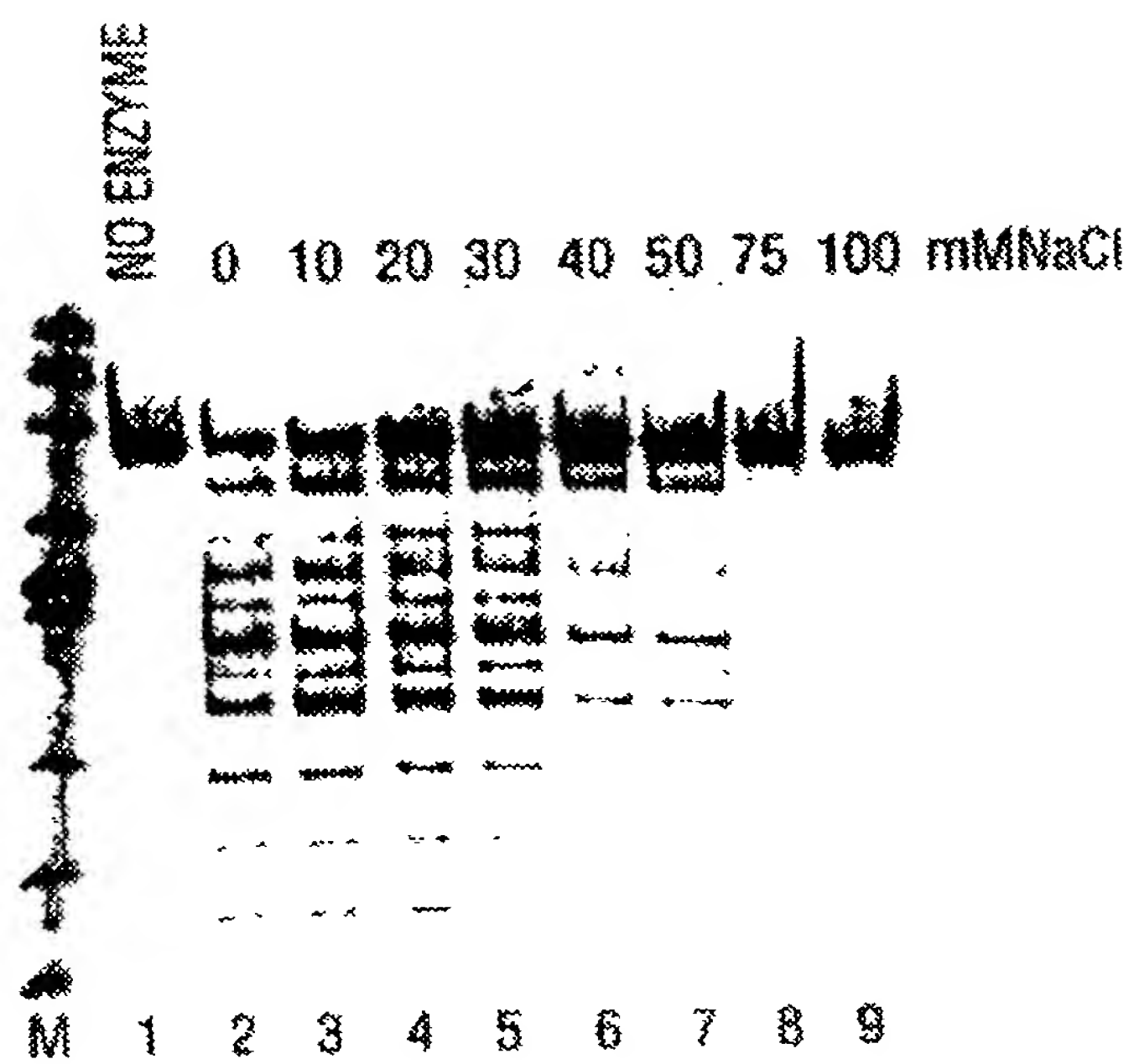


FIG. 52

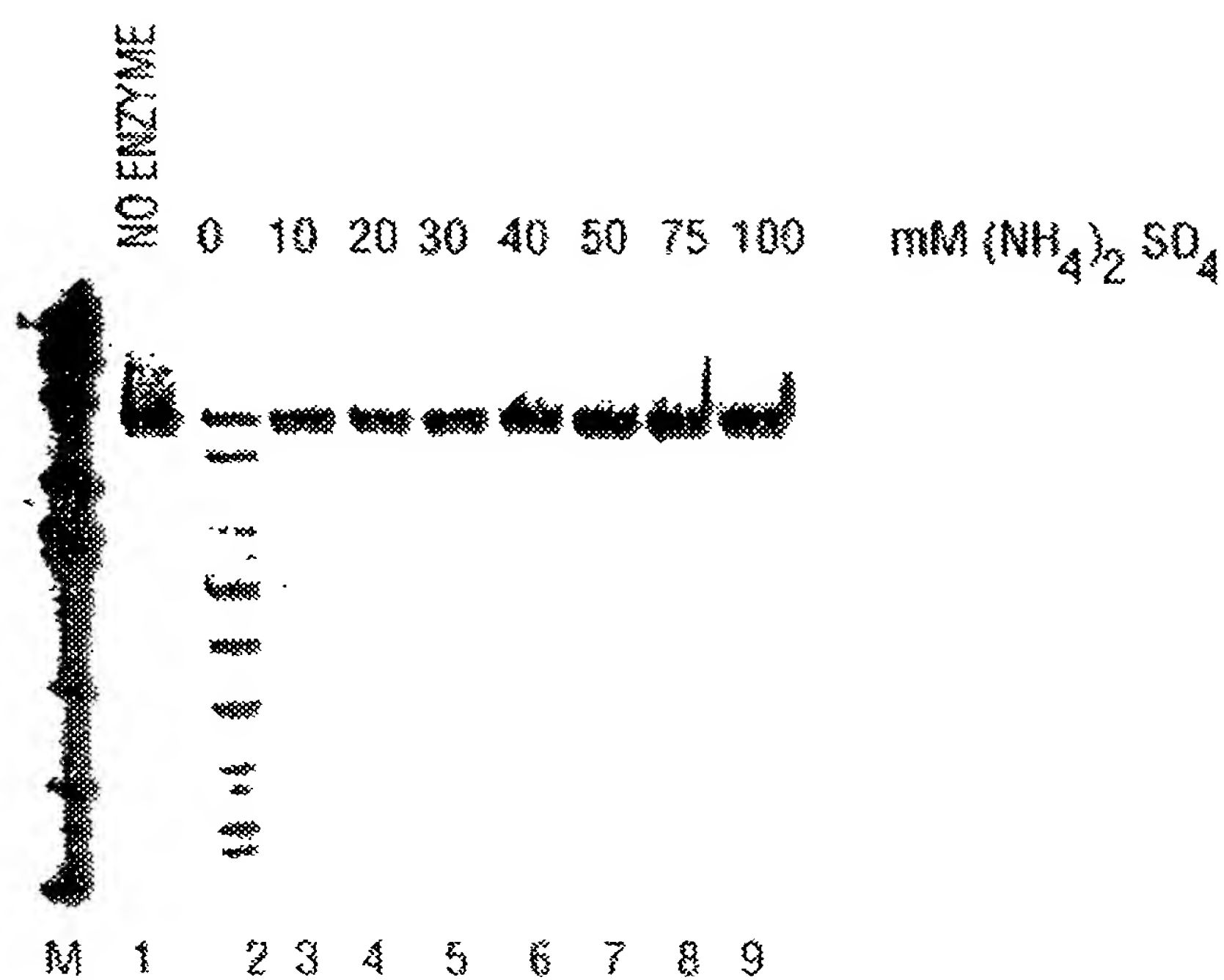


FIG. 53

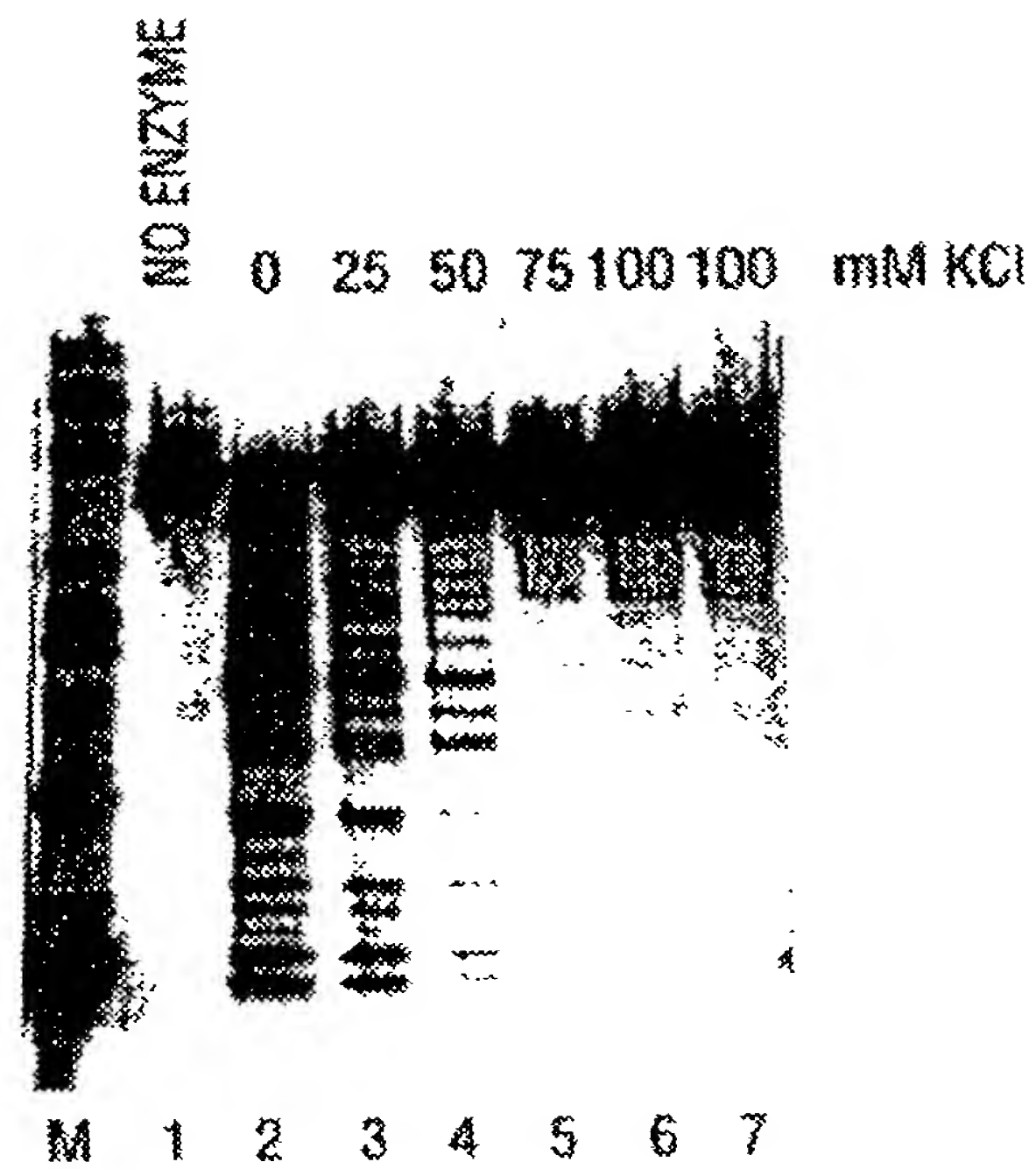


FIG. 54

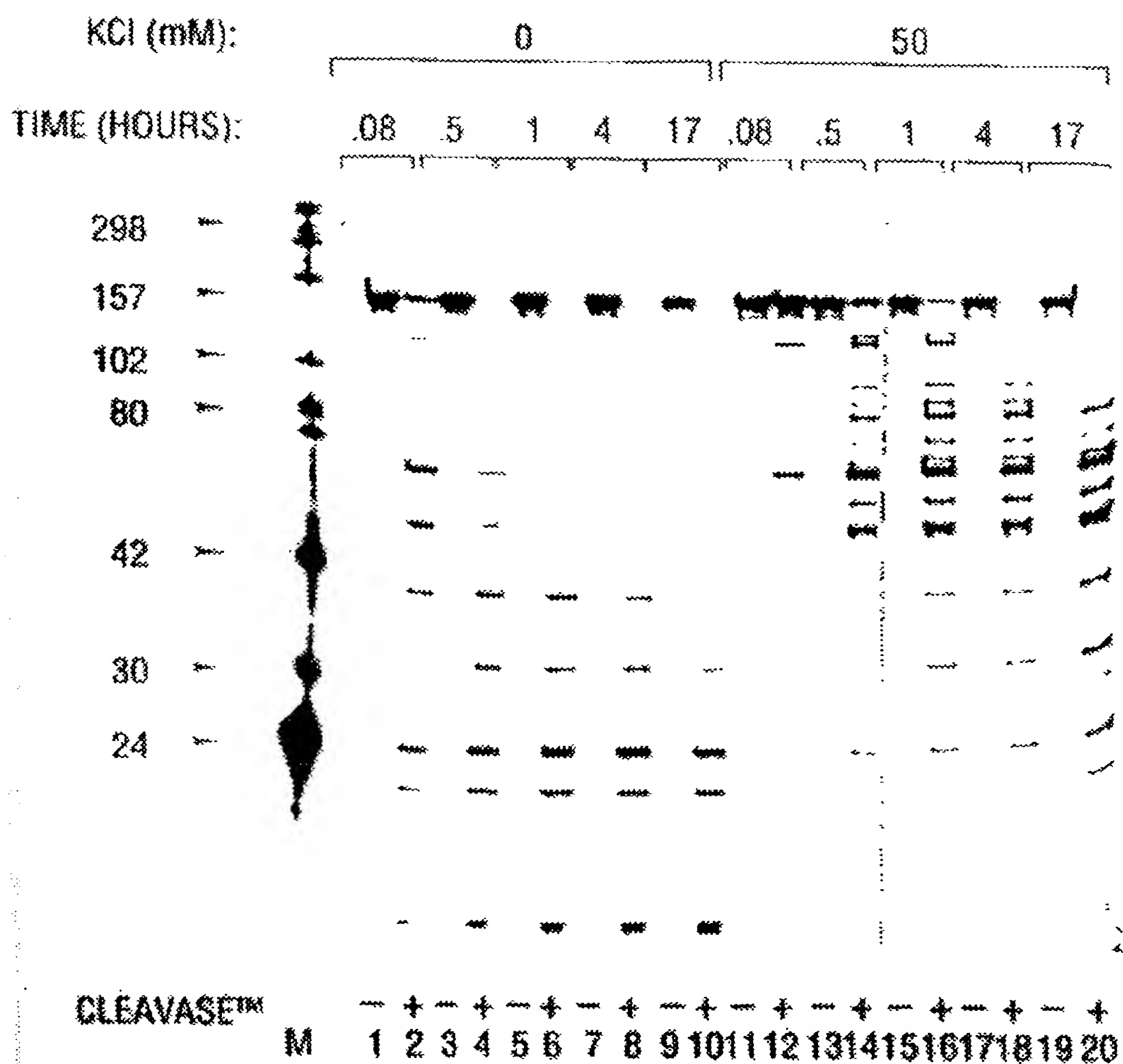


FIG. 55

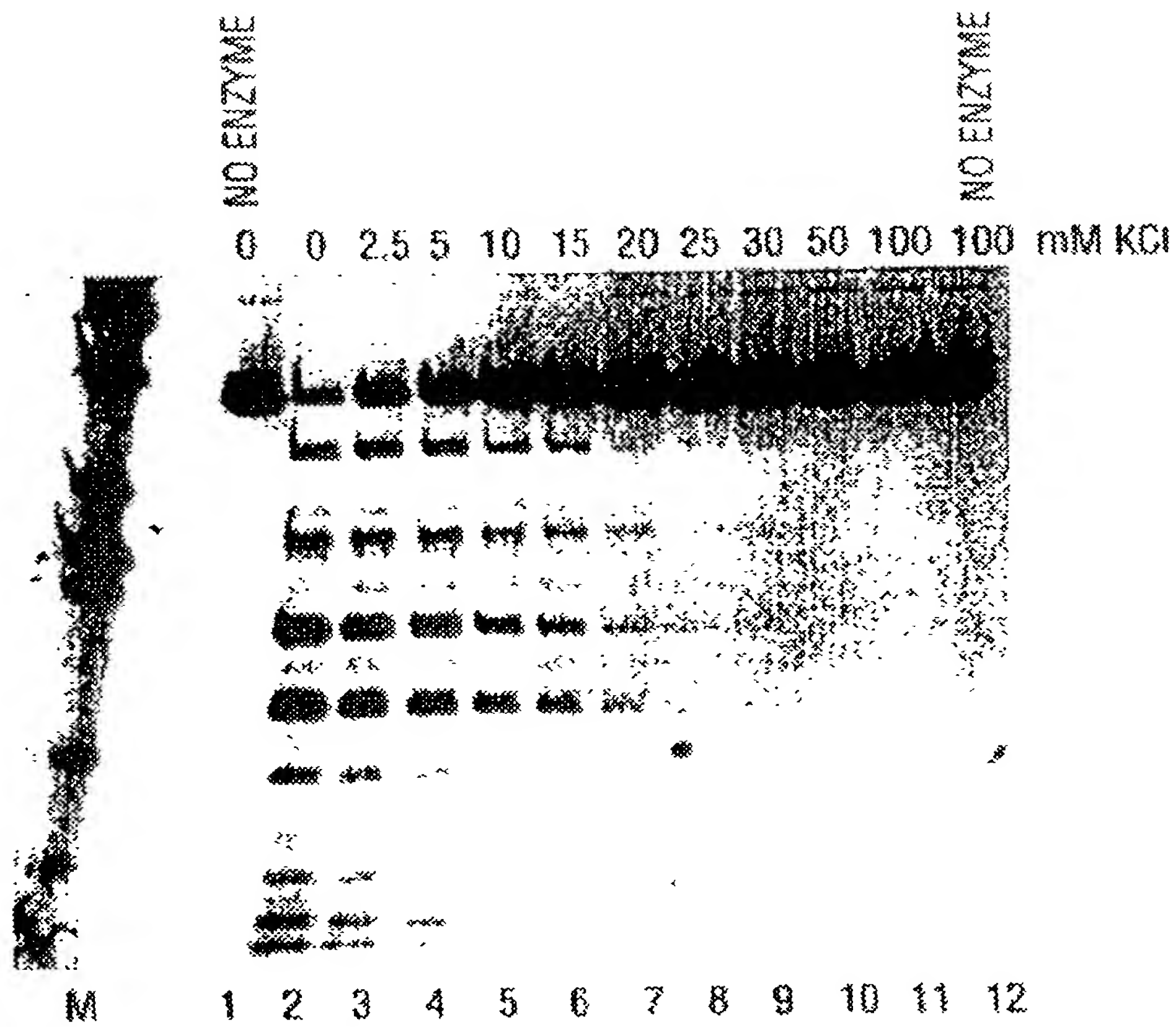


FIG. 57

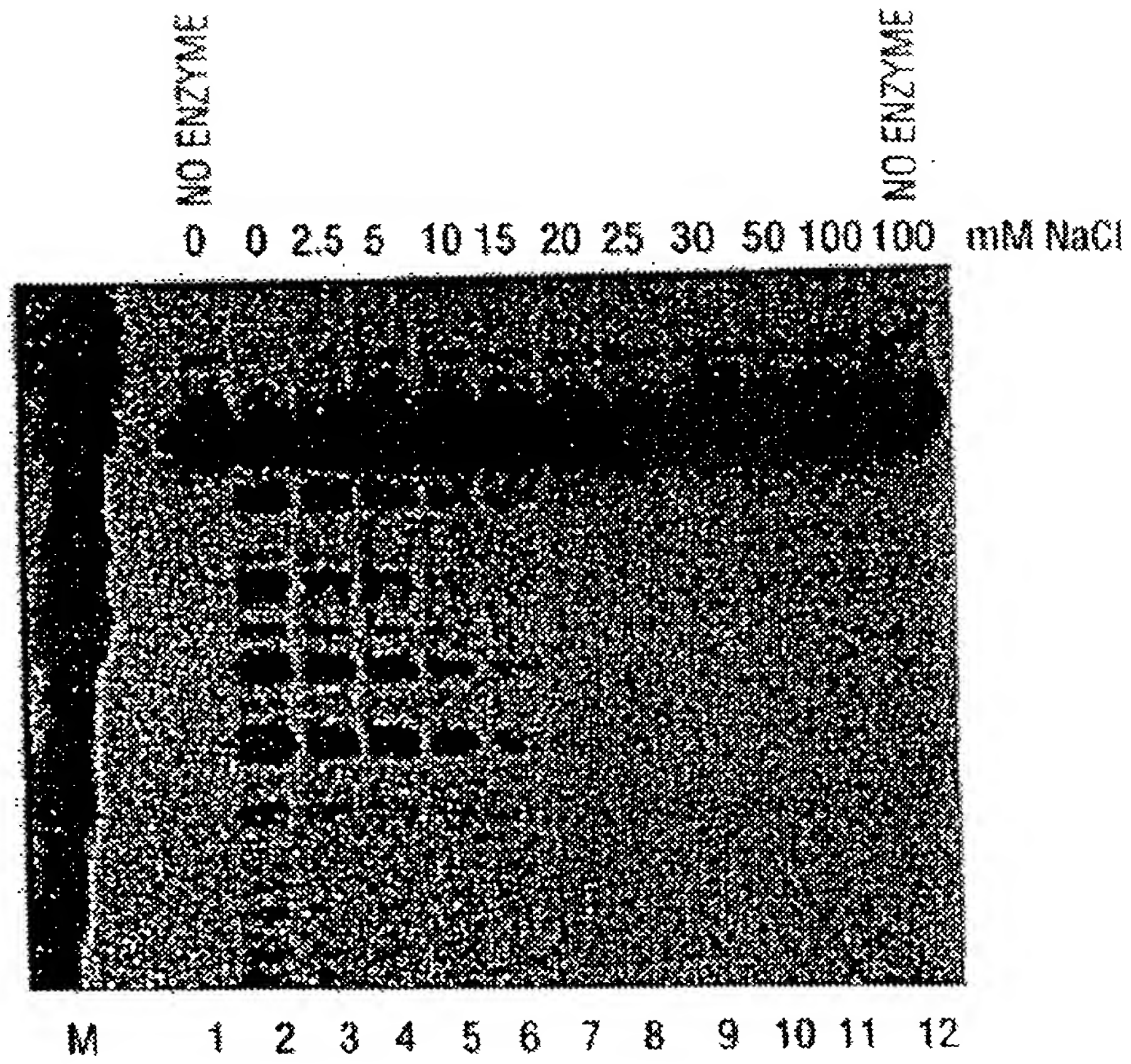


FIG. 58

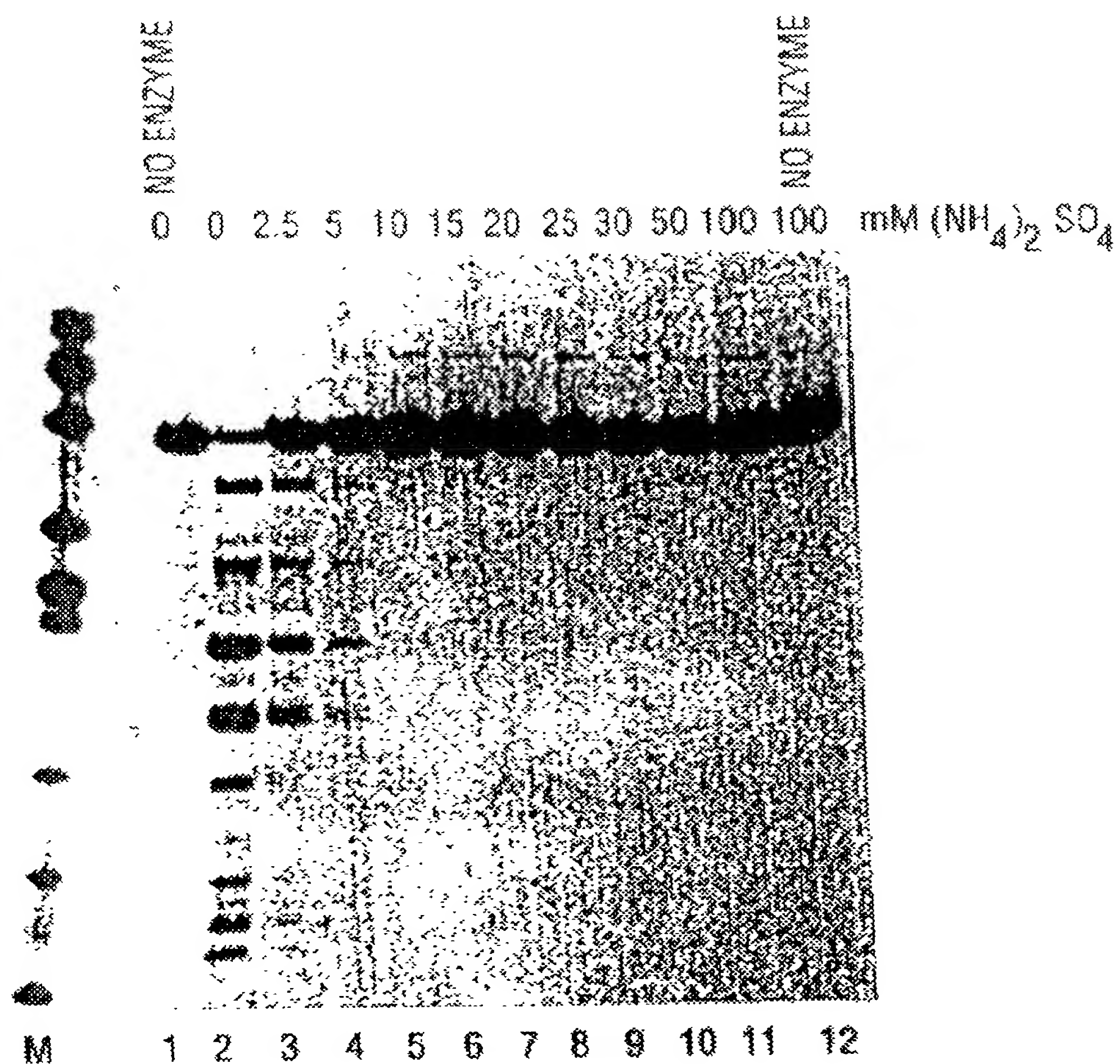


FIG. 59

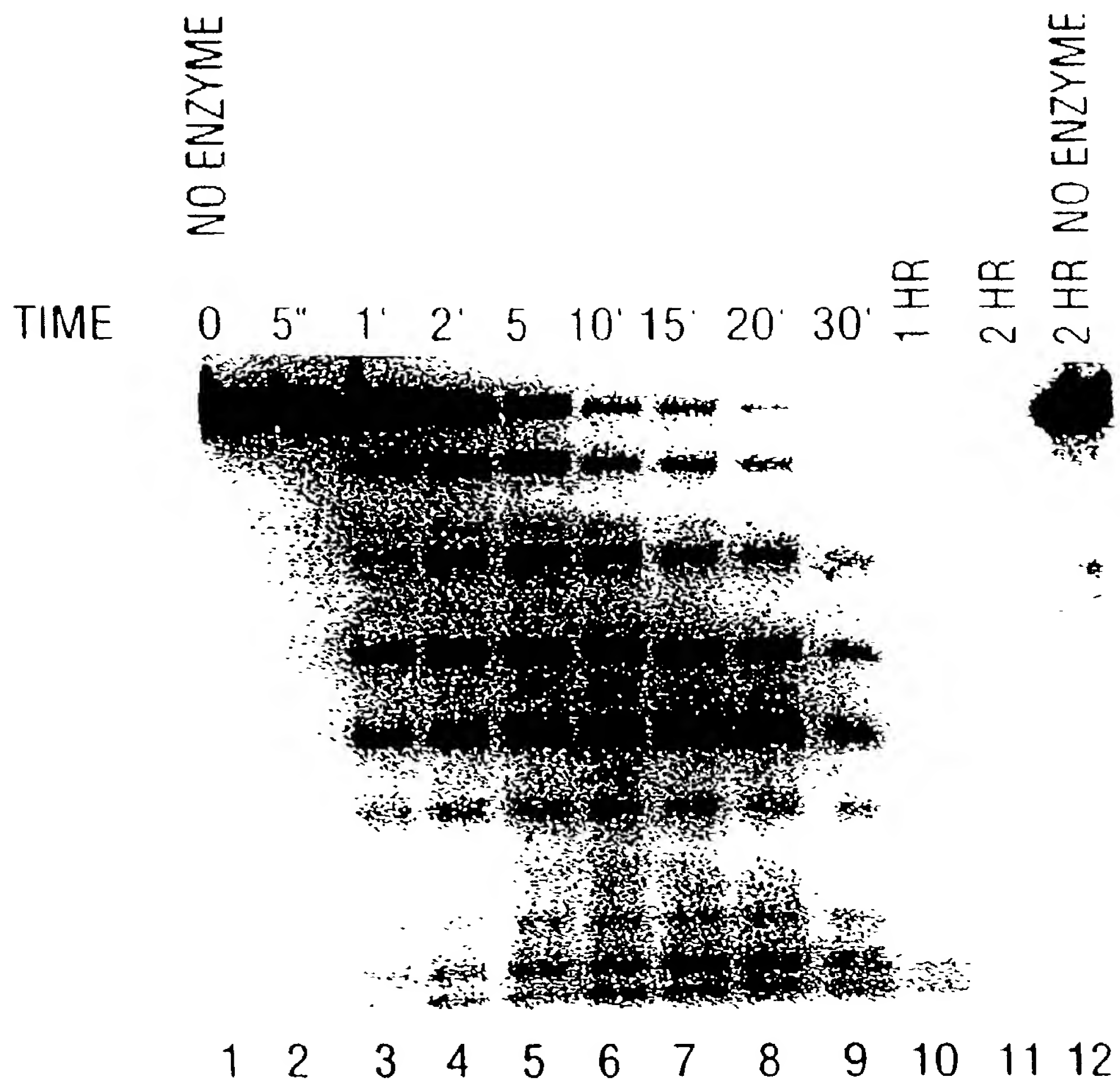


FIG. 60

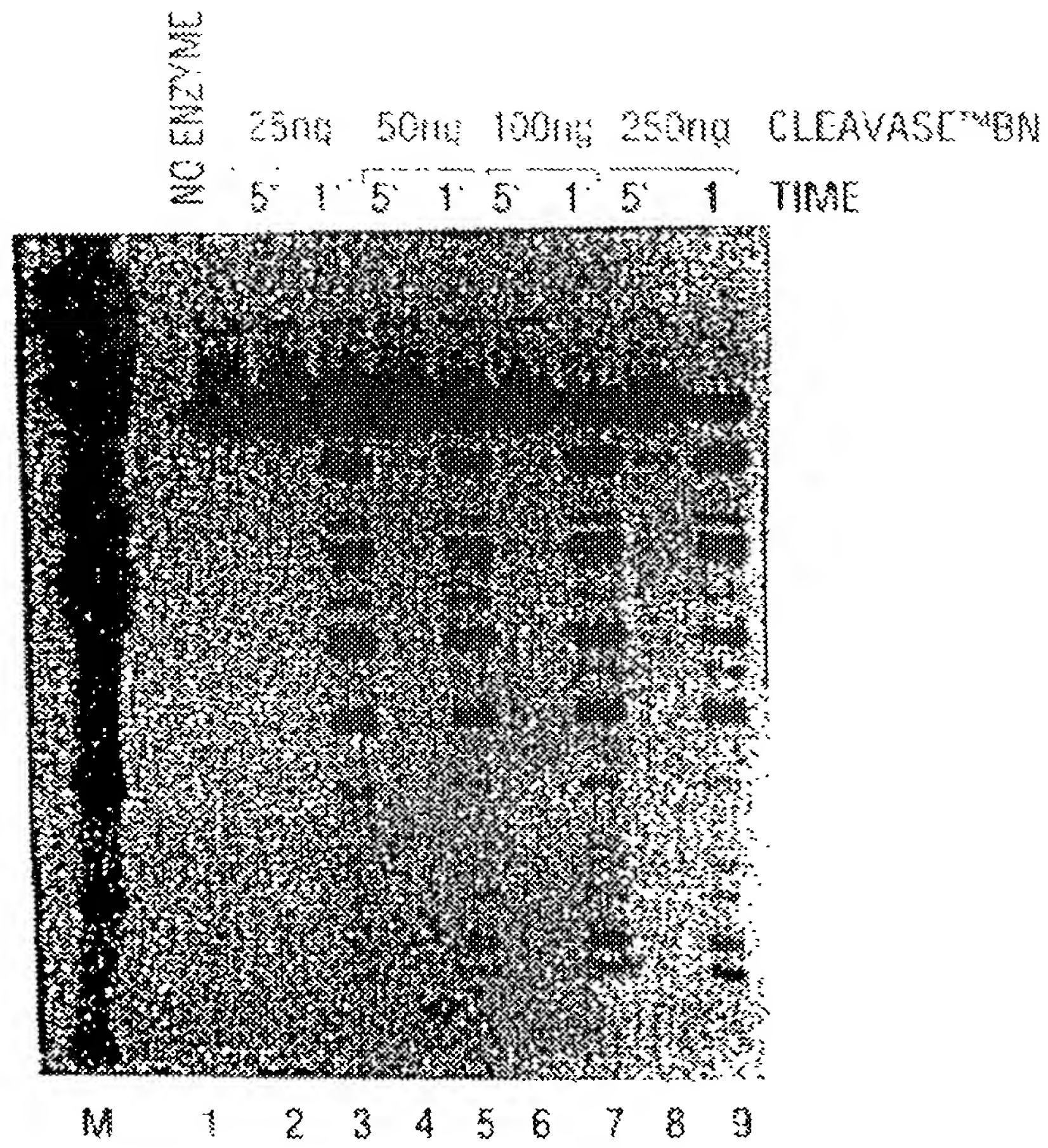


FIG. 61

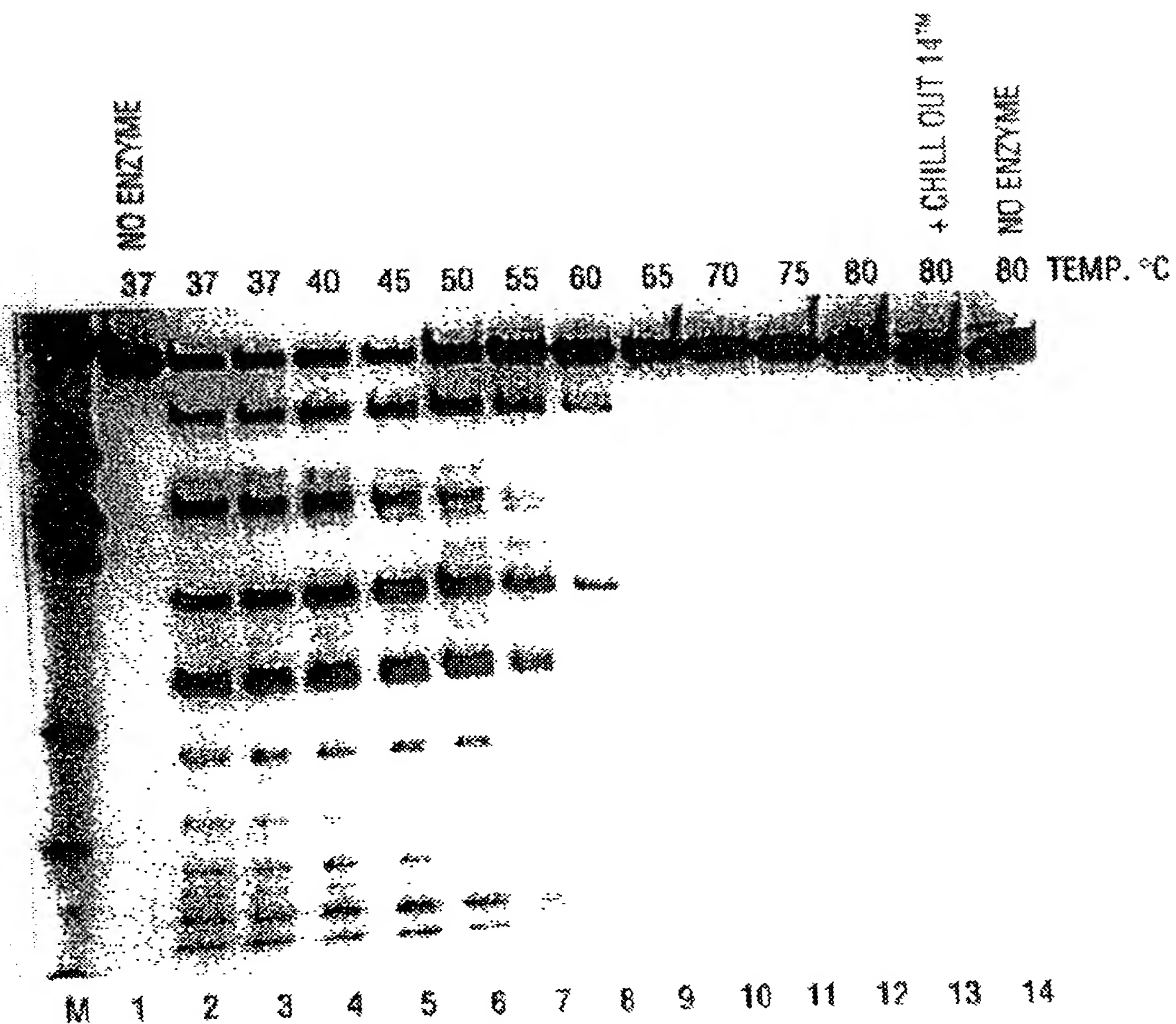


FIG. 62

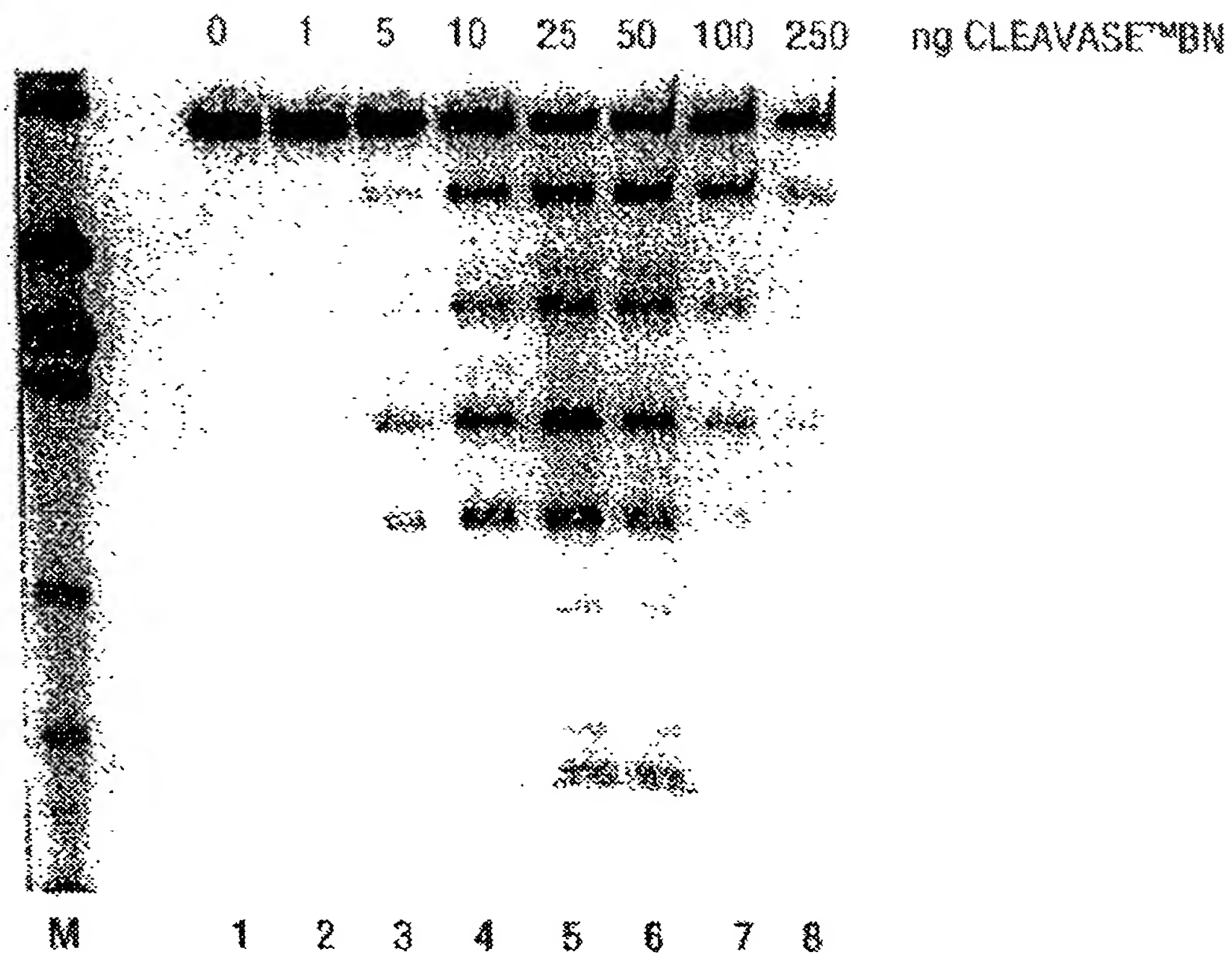


FIG. 63

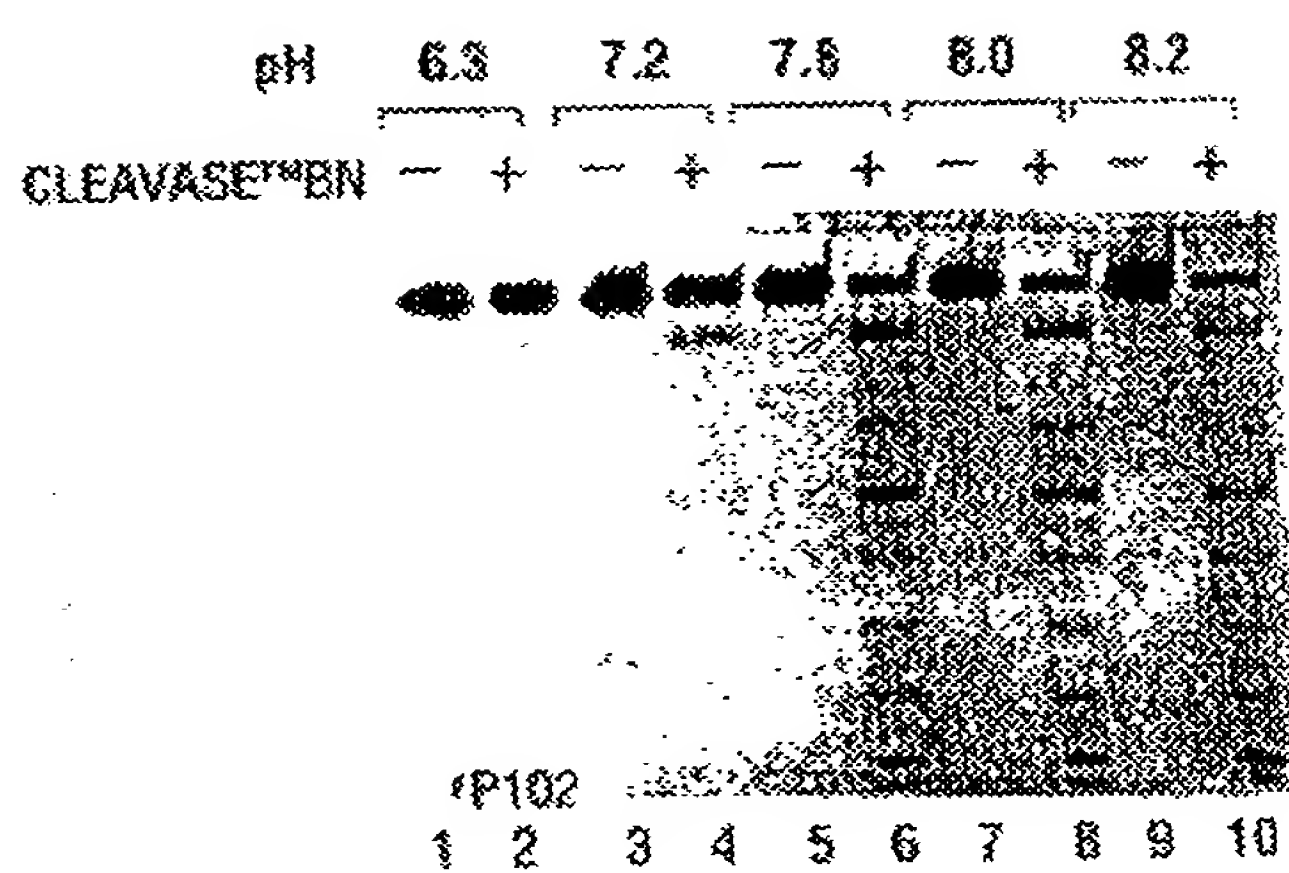


FIG. 64A

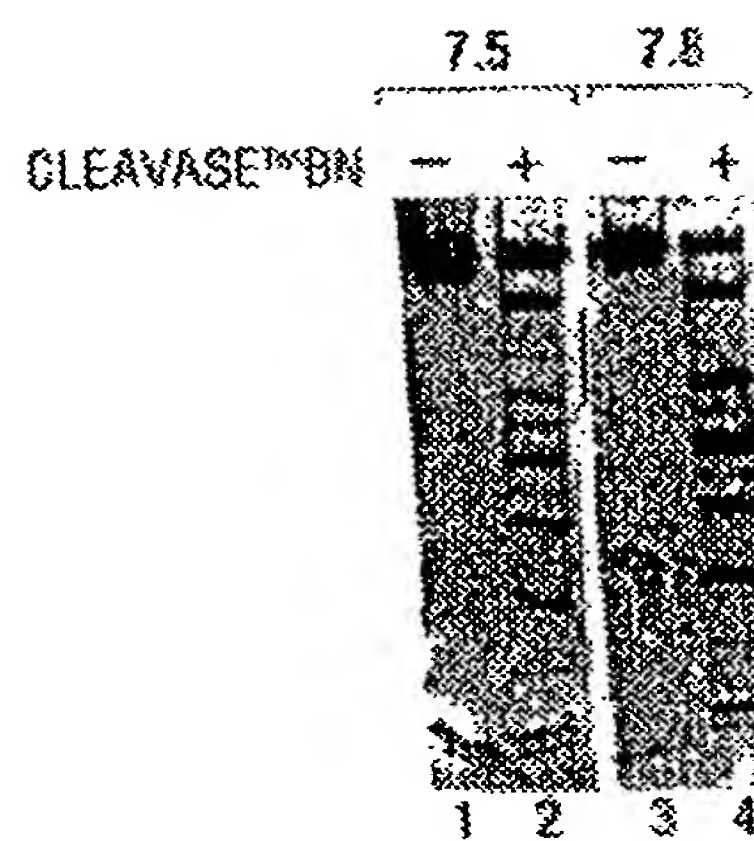


FIG. 64B

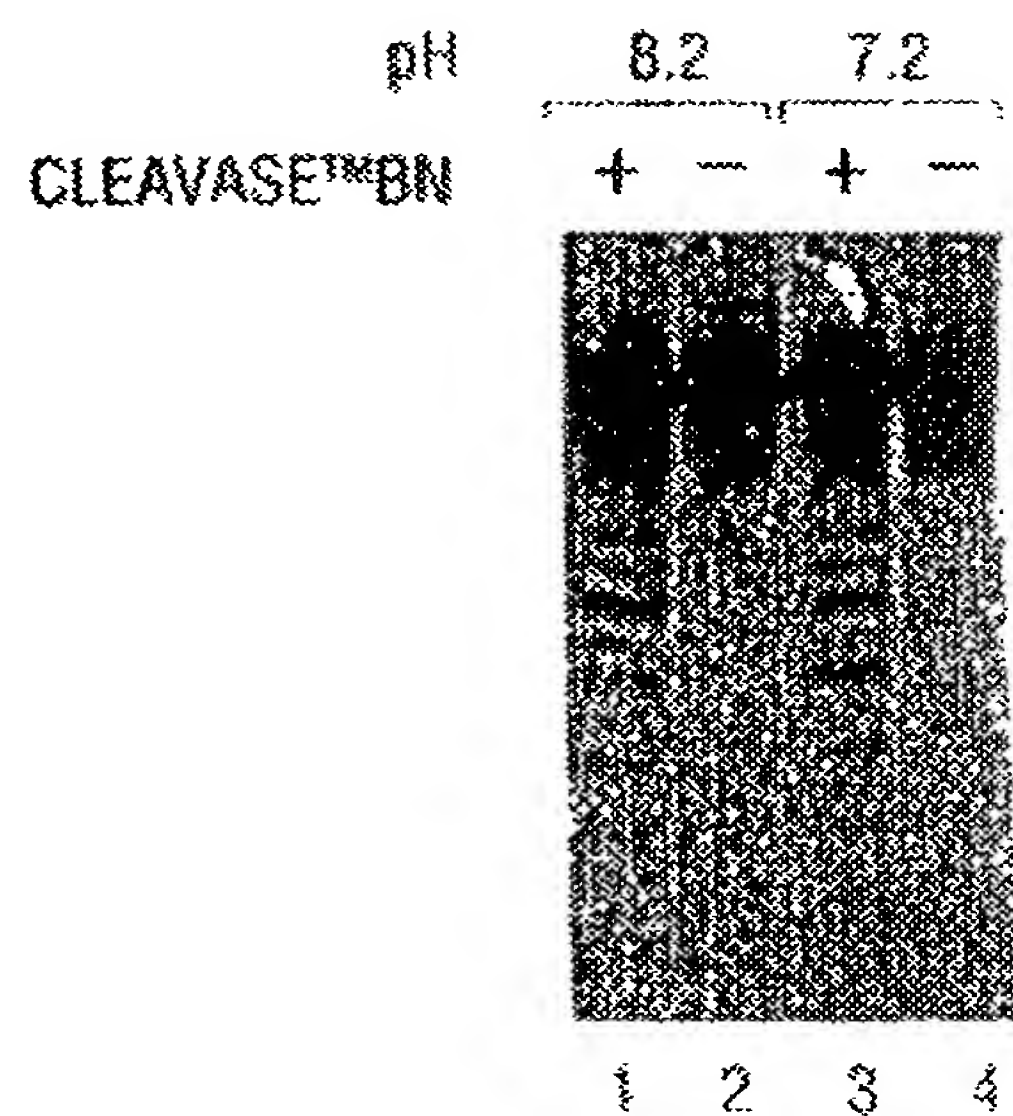


FIG. 65A

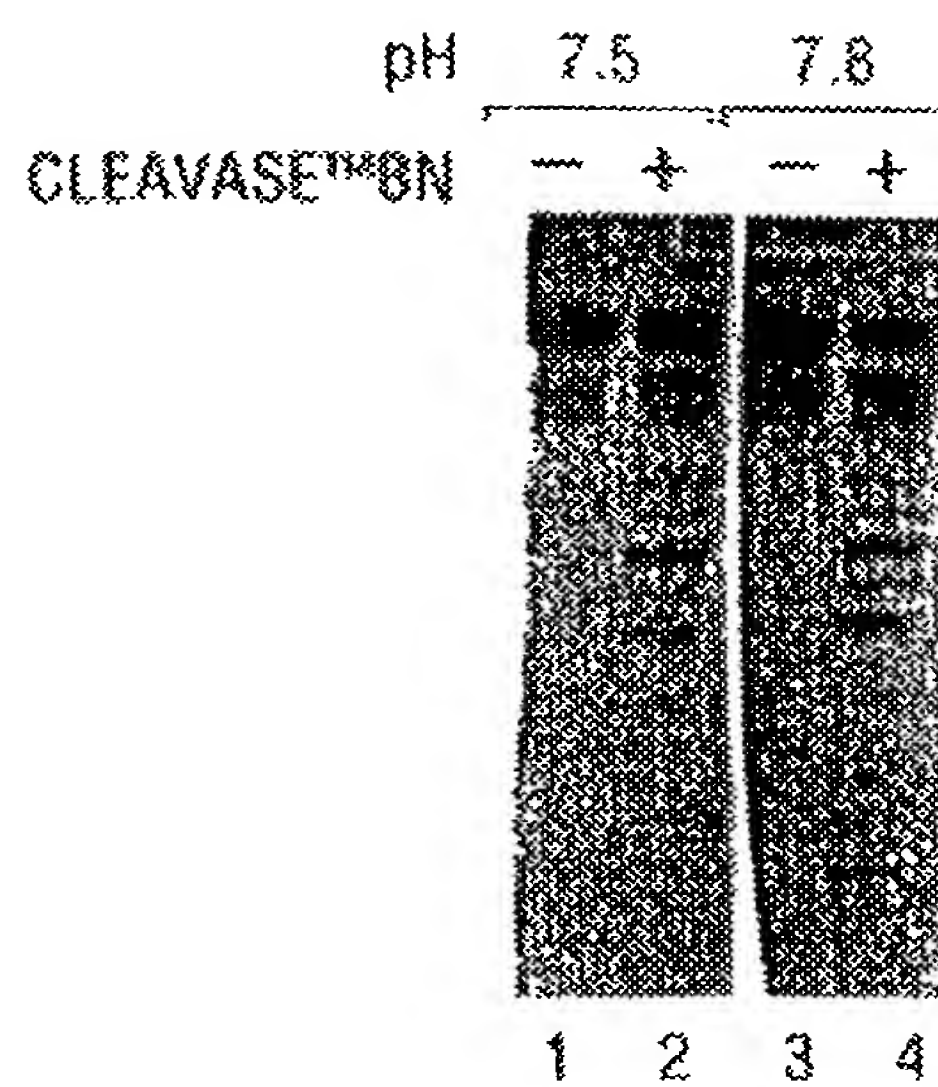


FIG. 65B

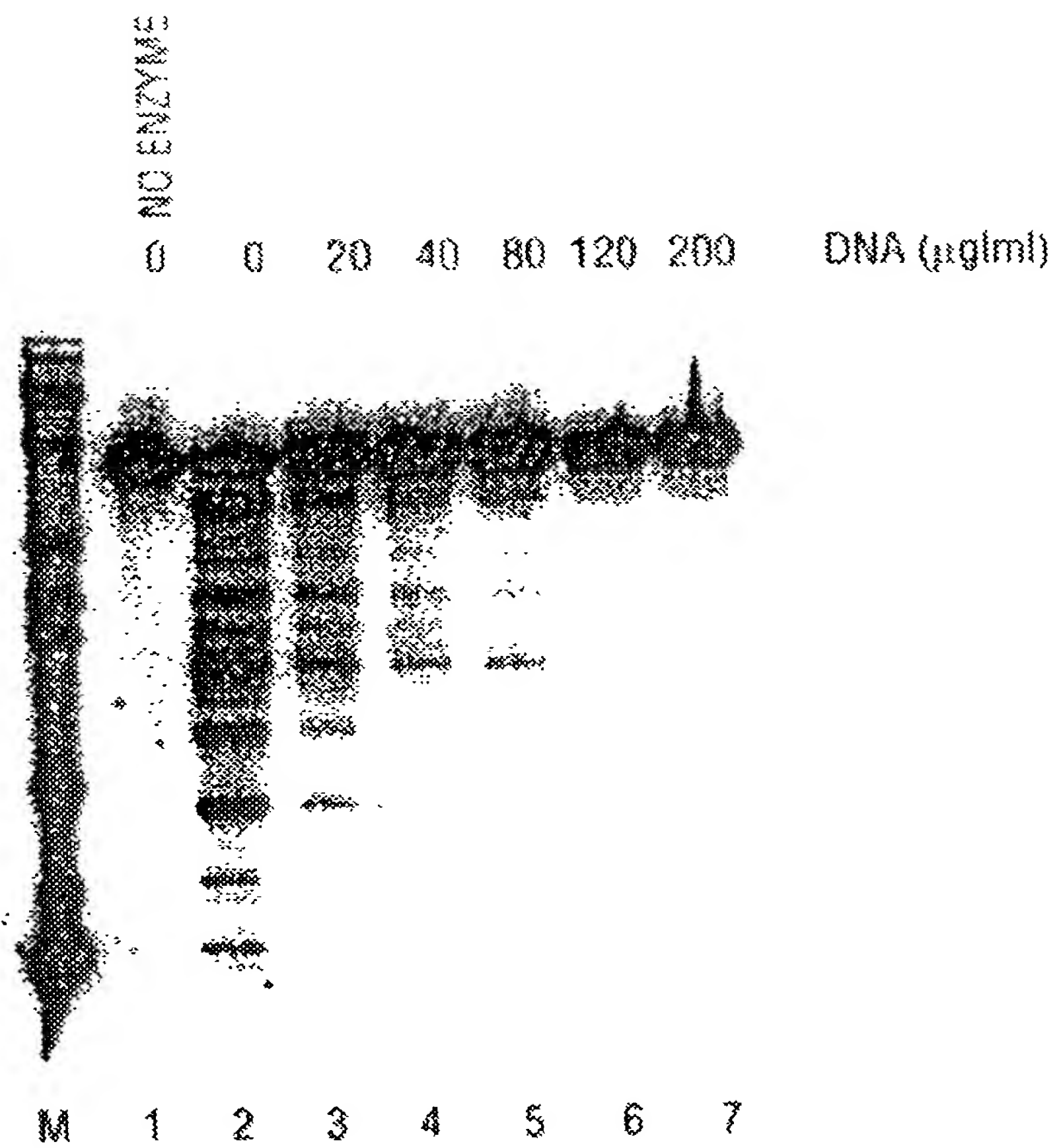


FIG. 66



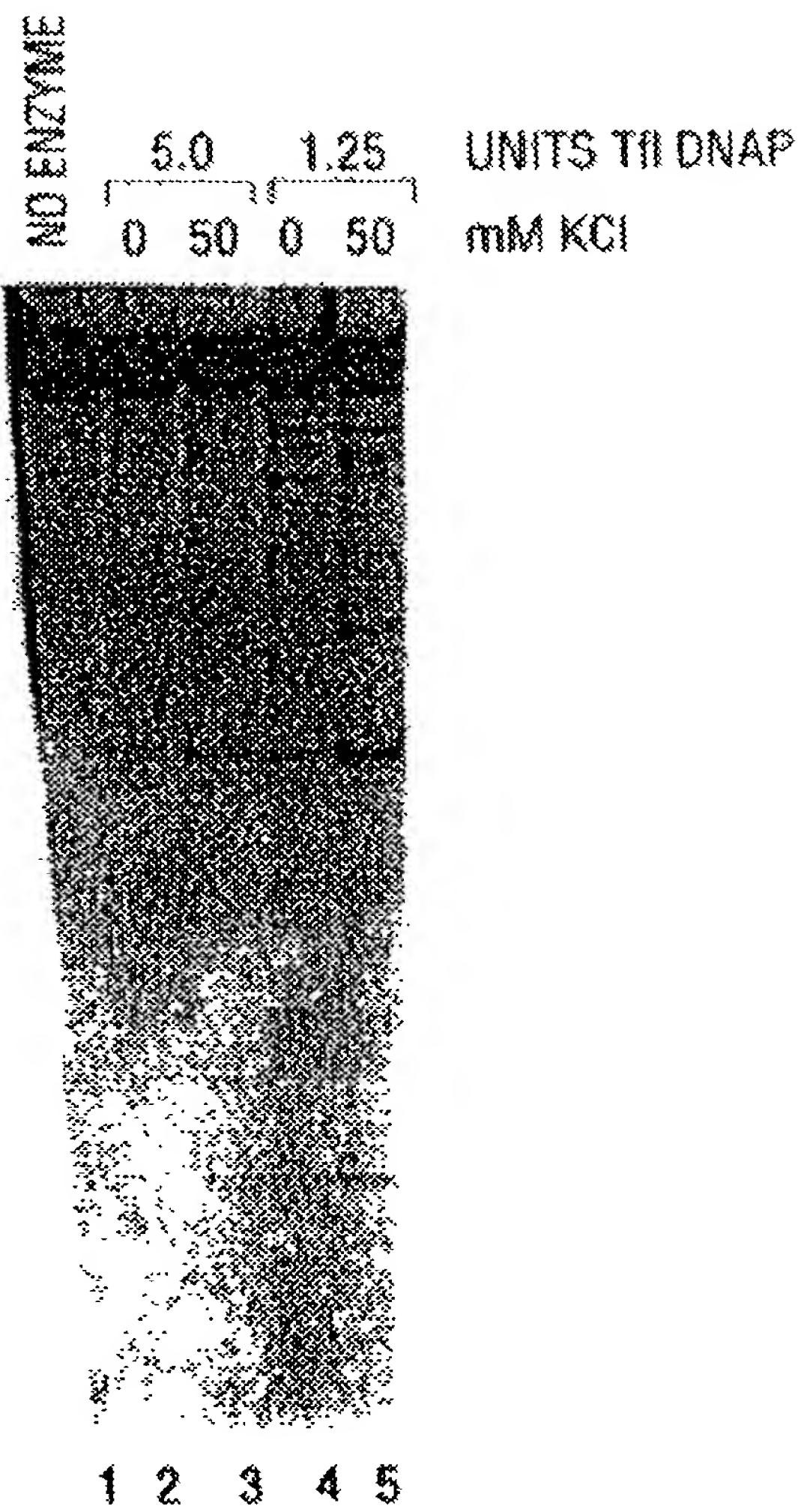


FIG. 67

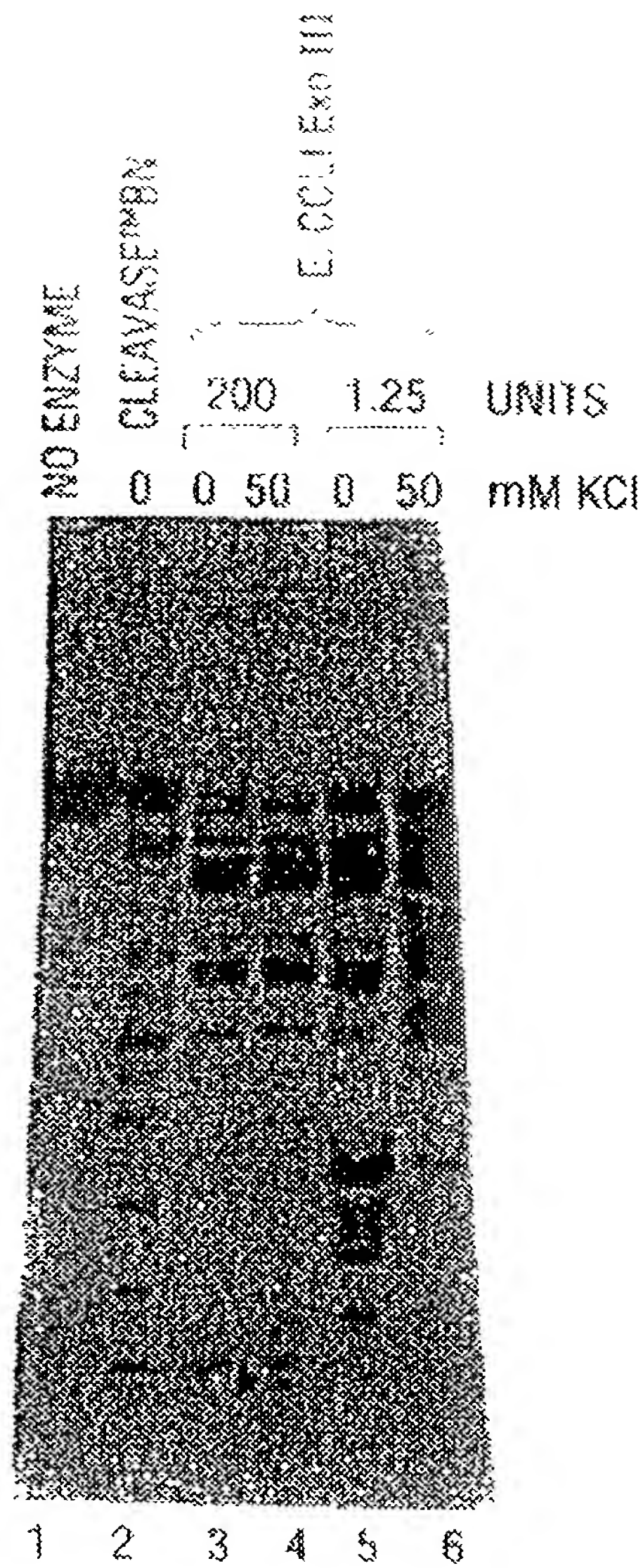


FIG. 69



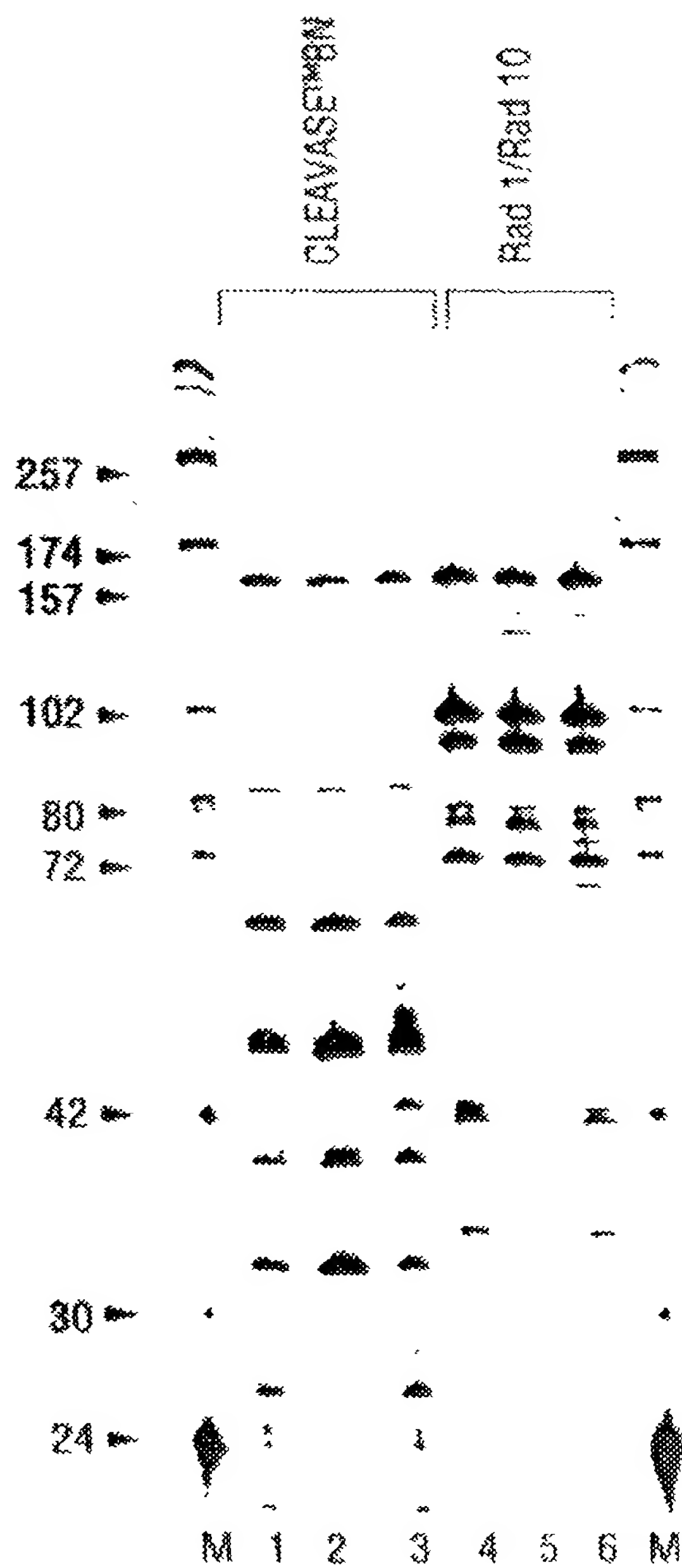


FIG. 72

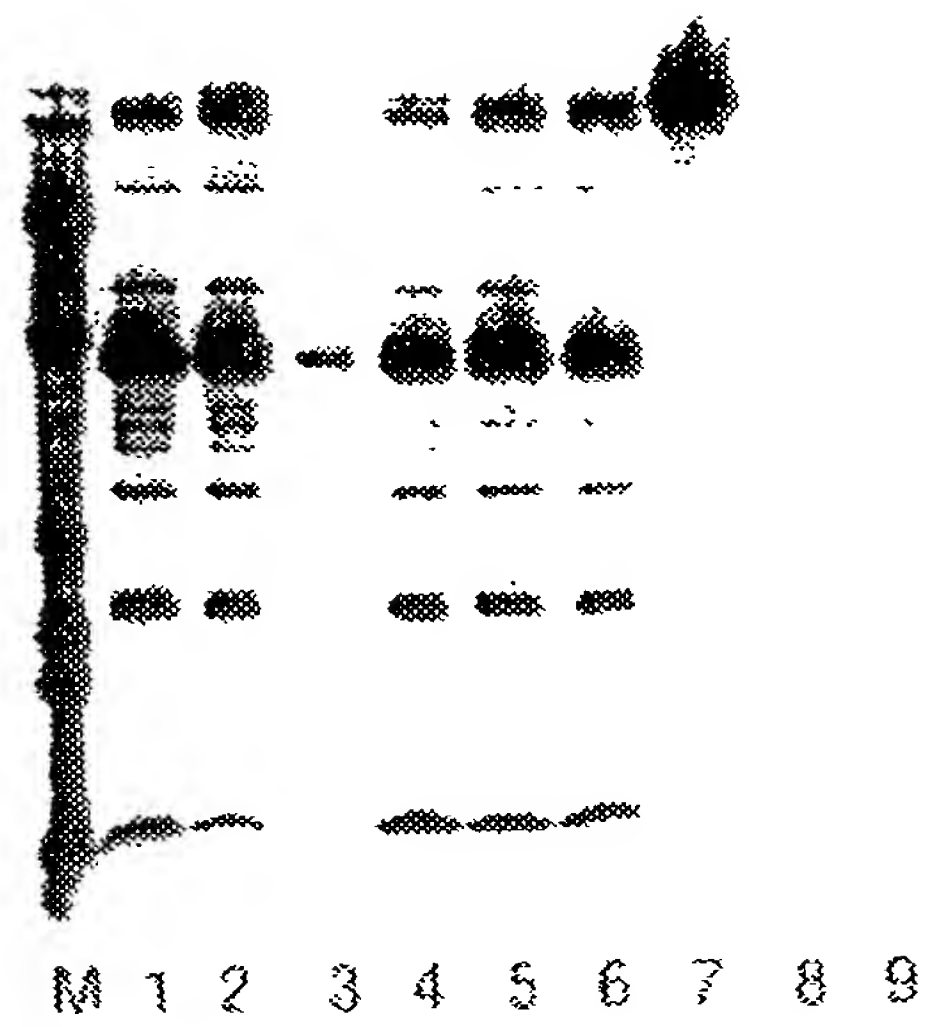
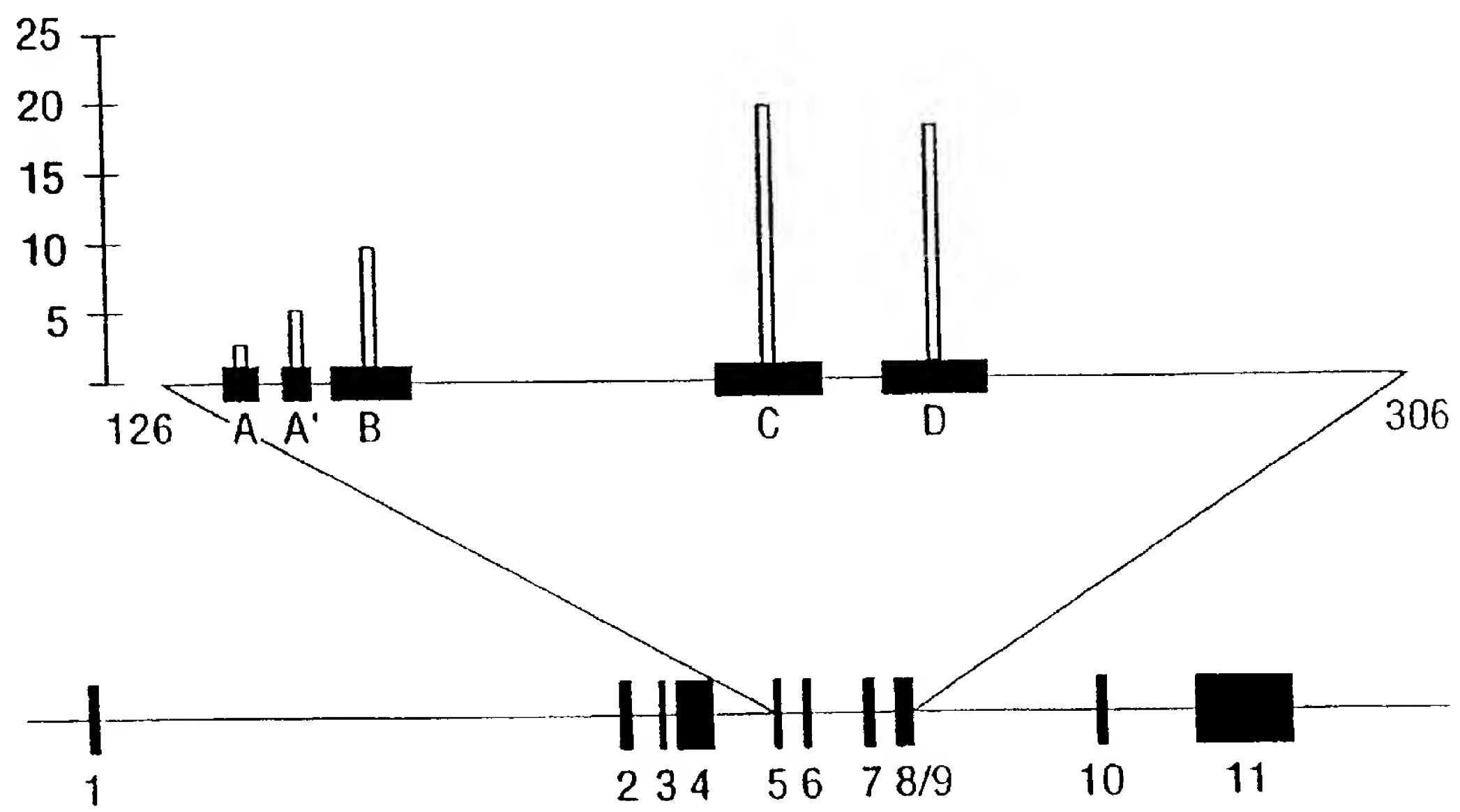


FIG. 75





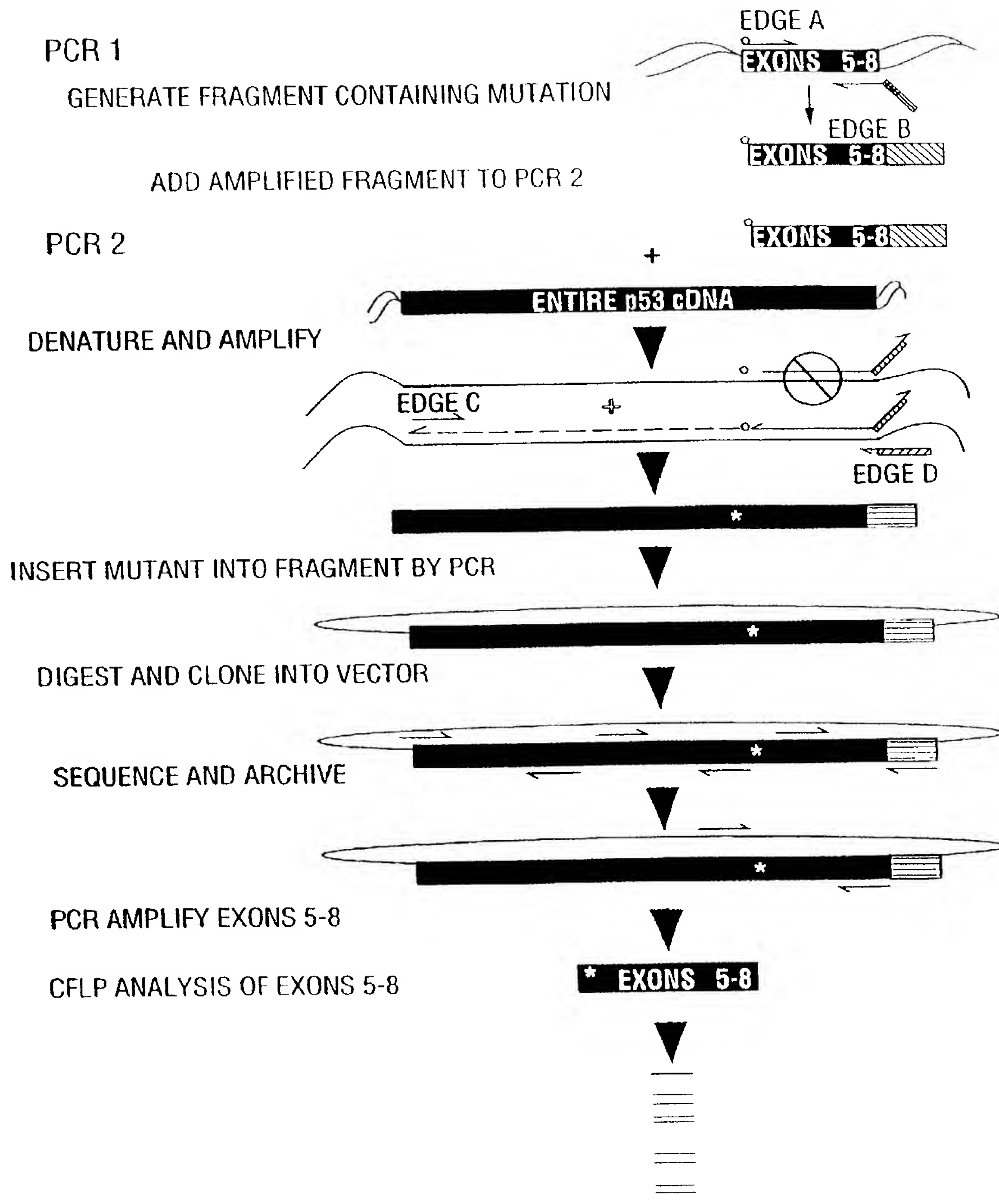


FIG. 77

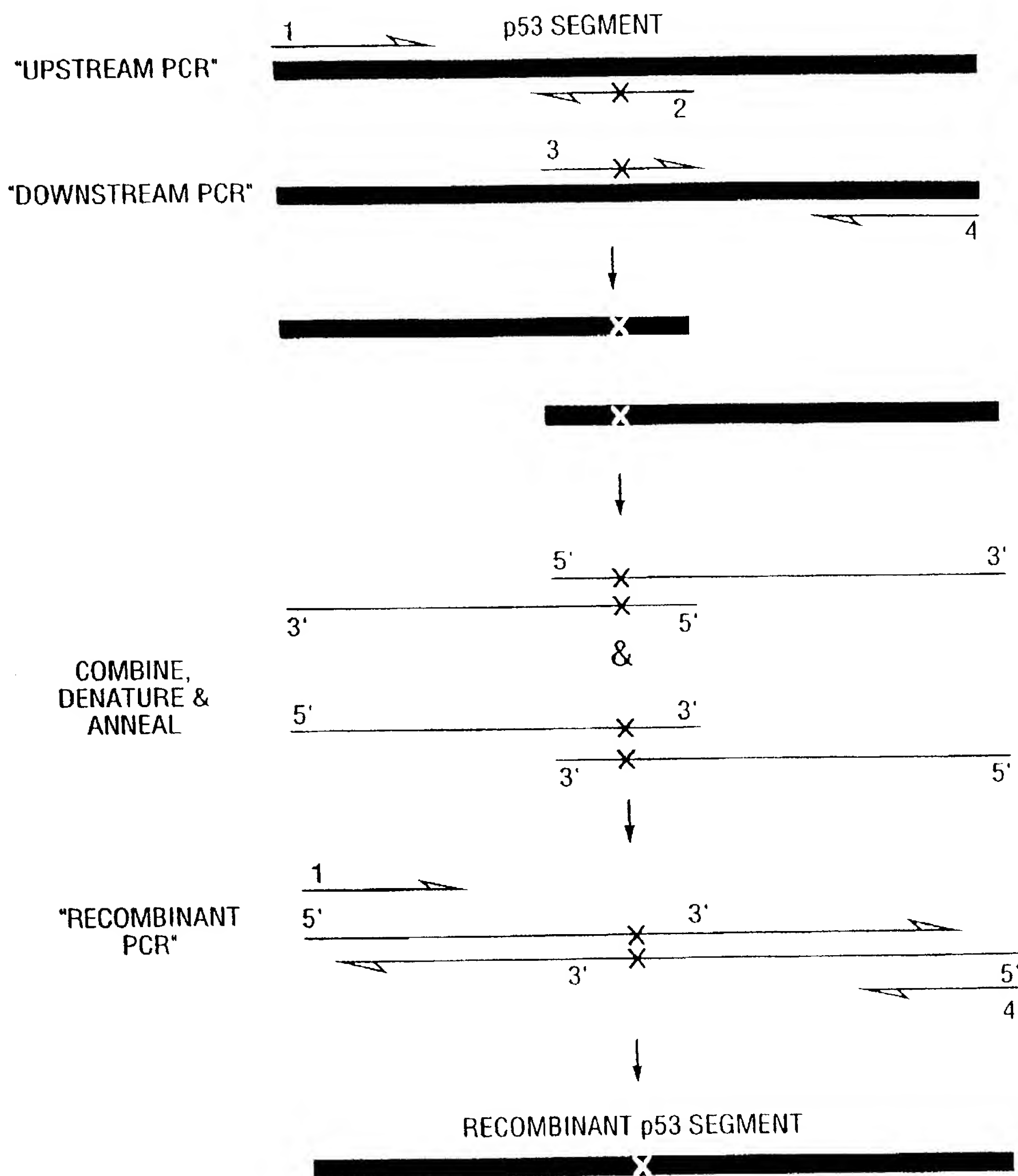


FIG. 78

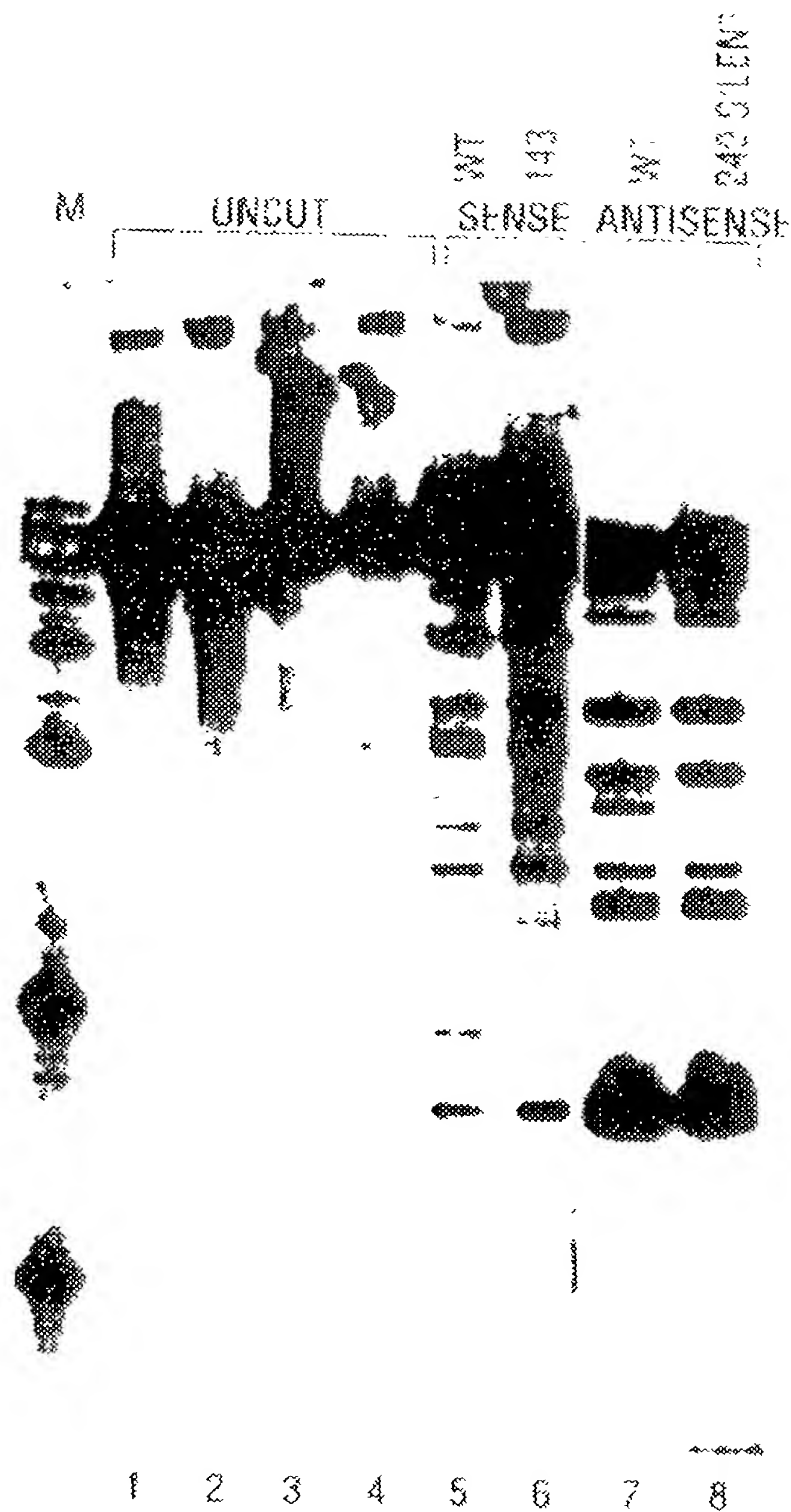


FIG. 79

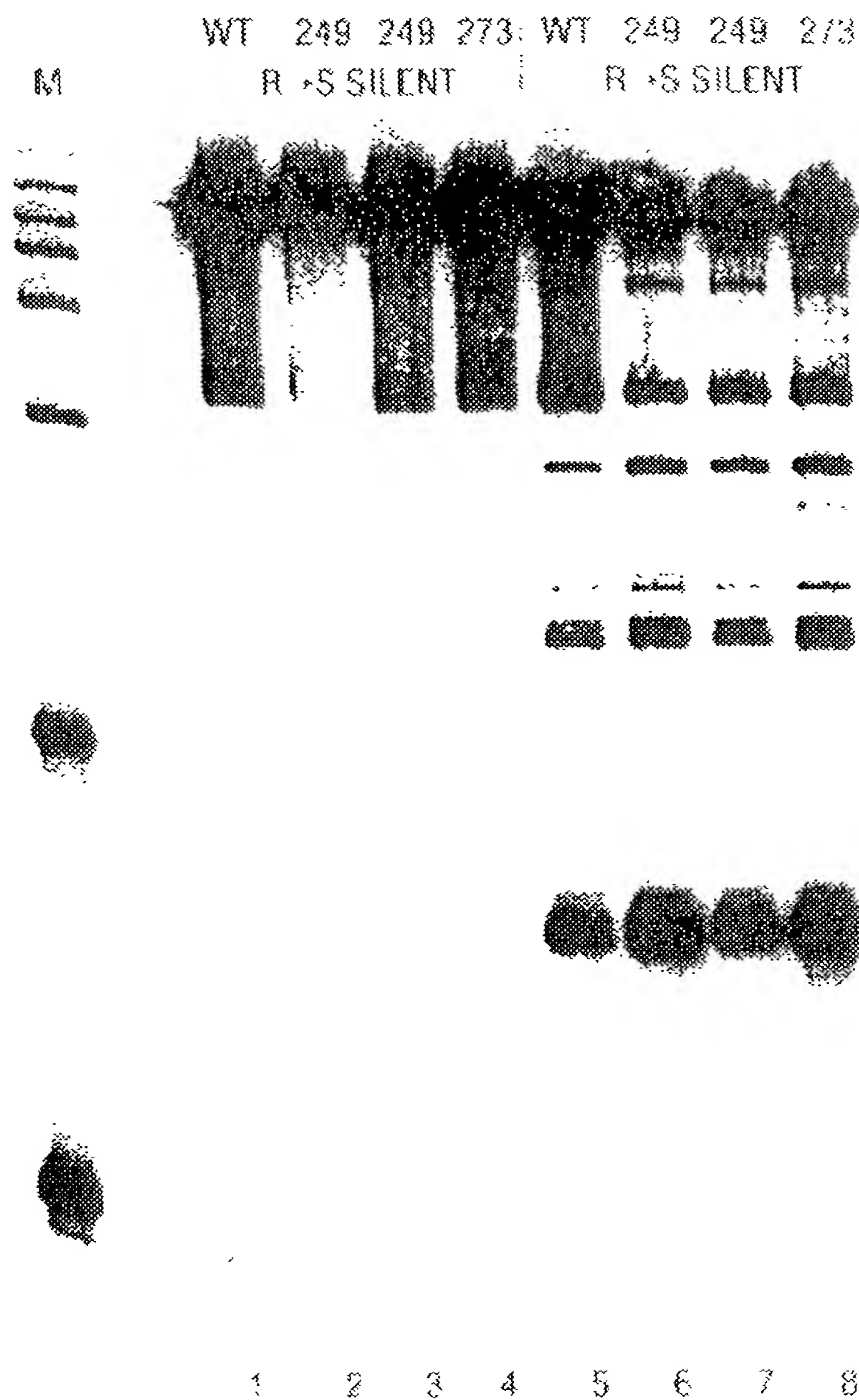


FIG. 80

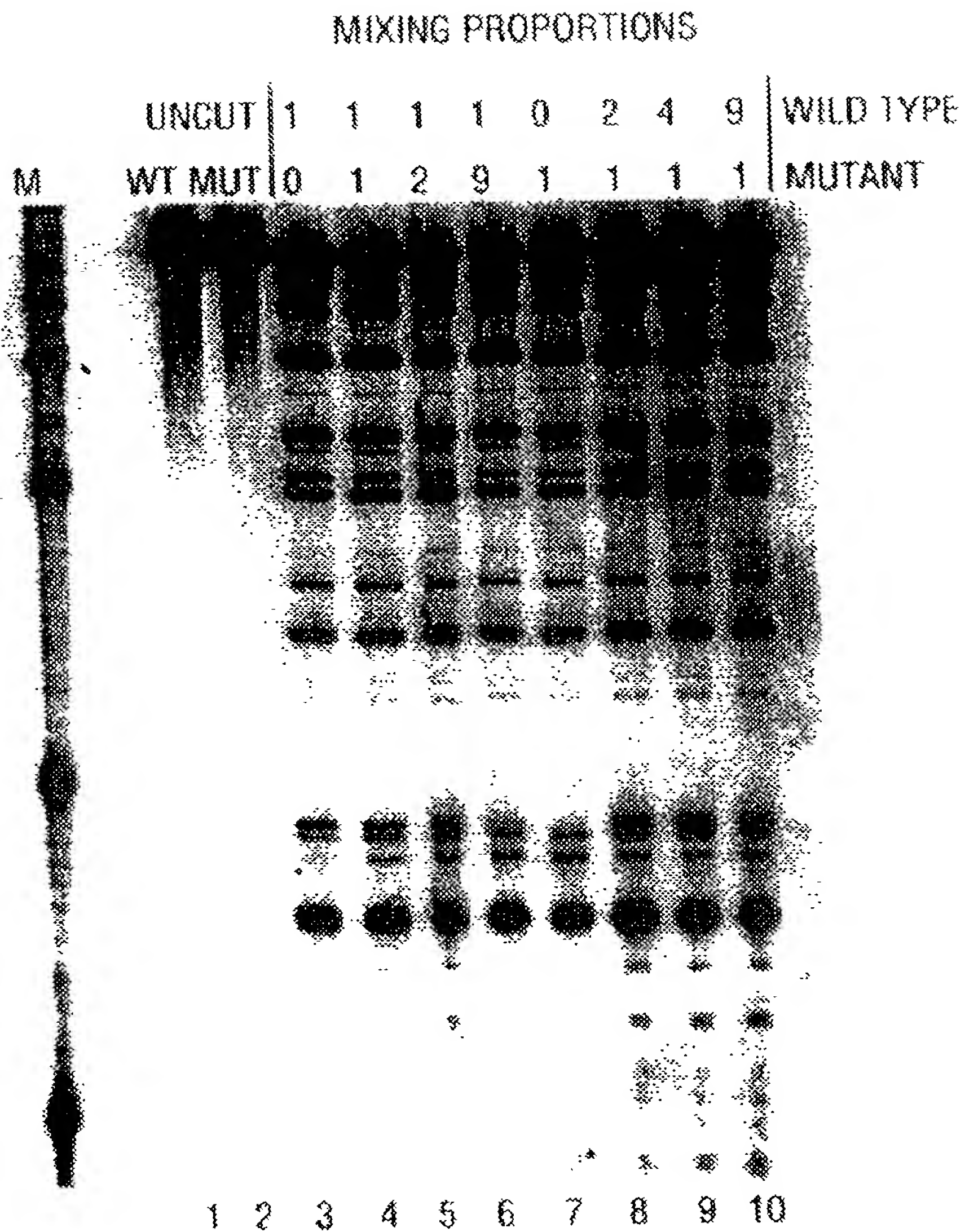


FIG. 81

HCVI.1	(SEQ	ID	N0:121)	1	CTGTCTTCCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCGTG	50
HCV2.1	(SEQ	ID	N0:122)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGTG	
HCV3.1	(SEQ	ID	N0:123)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGTG	
HCV4.2	(SEQ	ID	N0:124)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGTG	
HCV6.1	(SEQ	ID	N0:125)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGTG	
HCV7.1	(SEQ	ID	N0:126)		CTGTCTTCCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCGTG	
HCV1.1				51	CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	100
HCV2.1					CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV3.1					CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV4.2					CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV6.1					CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV7.1					CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV1.1				101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-AAA	150
HCV2.1					GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV3.1					GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV4.2					GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	GTGGATGIAA	
HCV6.1					GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-AAA	
HCV7.1					GGTGAGTACA	CCGGAATCGC	TGGGTTGACC	GGGTCCTTTC	TTGGAG-CAA	

FIG. 82A

HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCCGGCCAT	TTGGGCGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGGTGC	CCCCGCGAGA	ICACTAGCCG	
HCV1.1	201	AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTTGG	TACTGCCCTGA	TAGGGTGCTT	250
HCV2.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTTG	GGTIGCGAAA	GGCCTTGTTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTTG	GGTCGCCGAAA	GGCCTTGTTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV1.1	251	GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		

FIG. 82B

39910323 032503

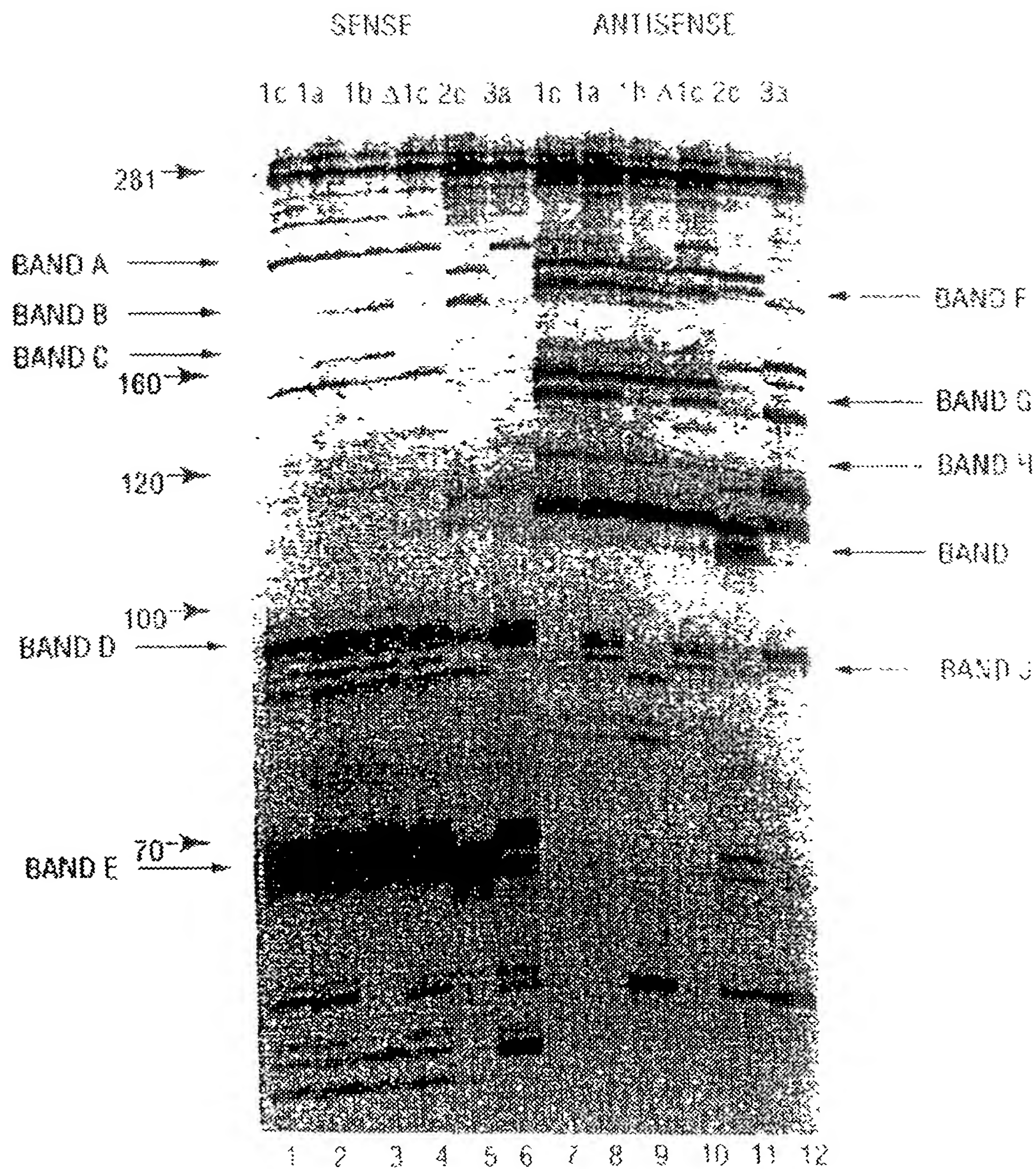


FIG. 83

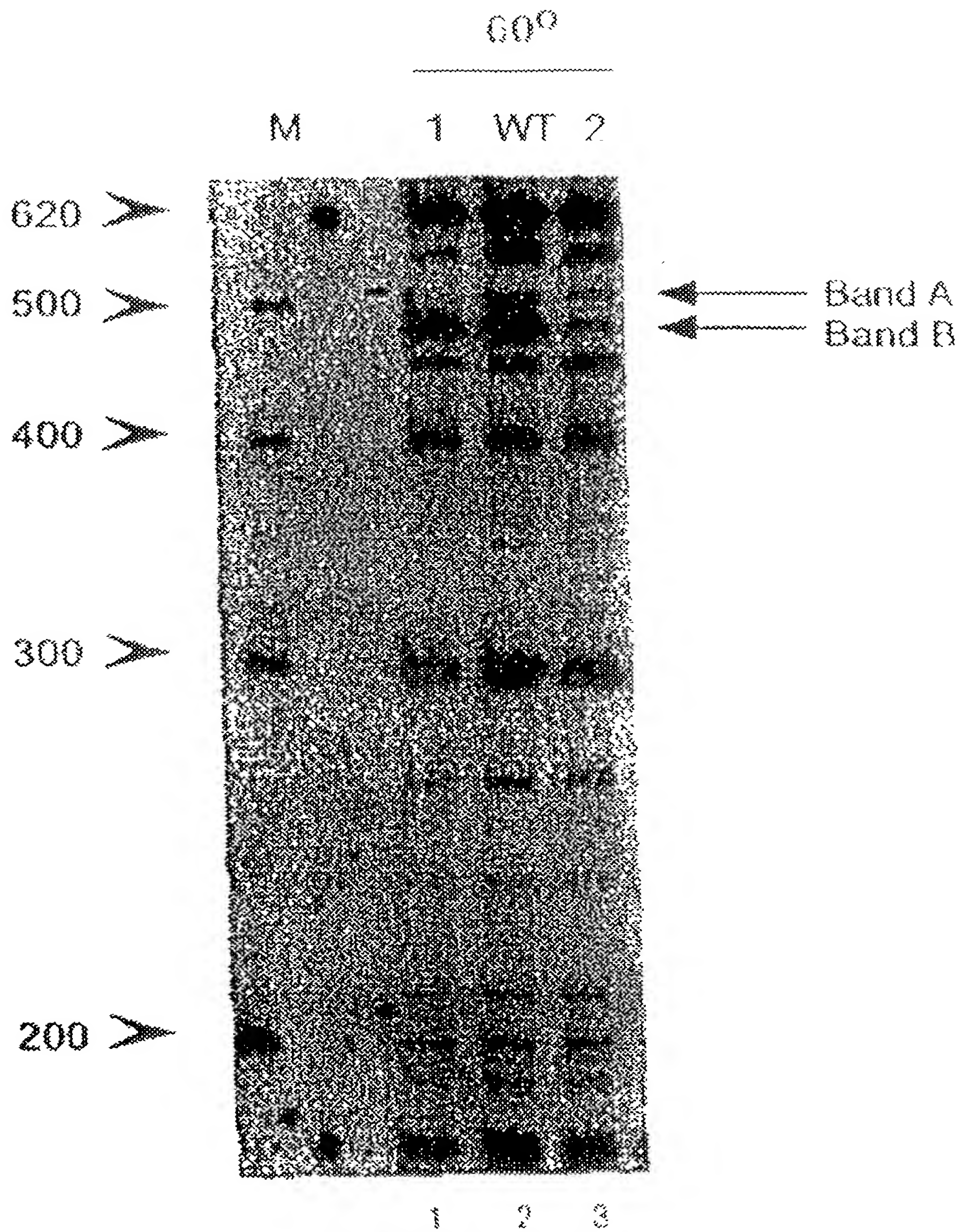
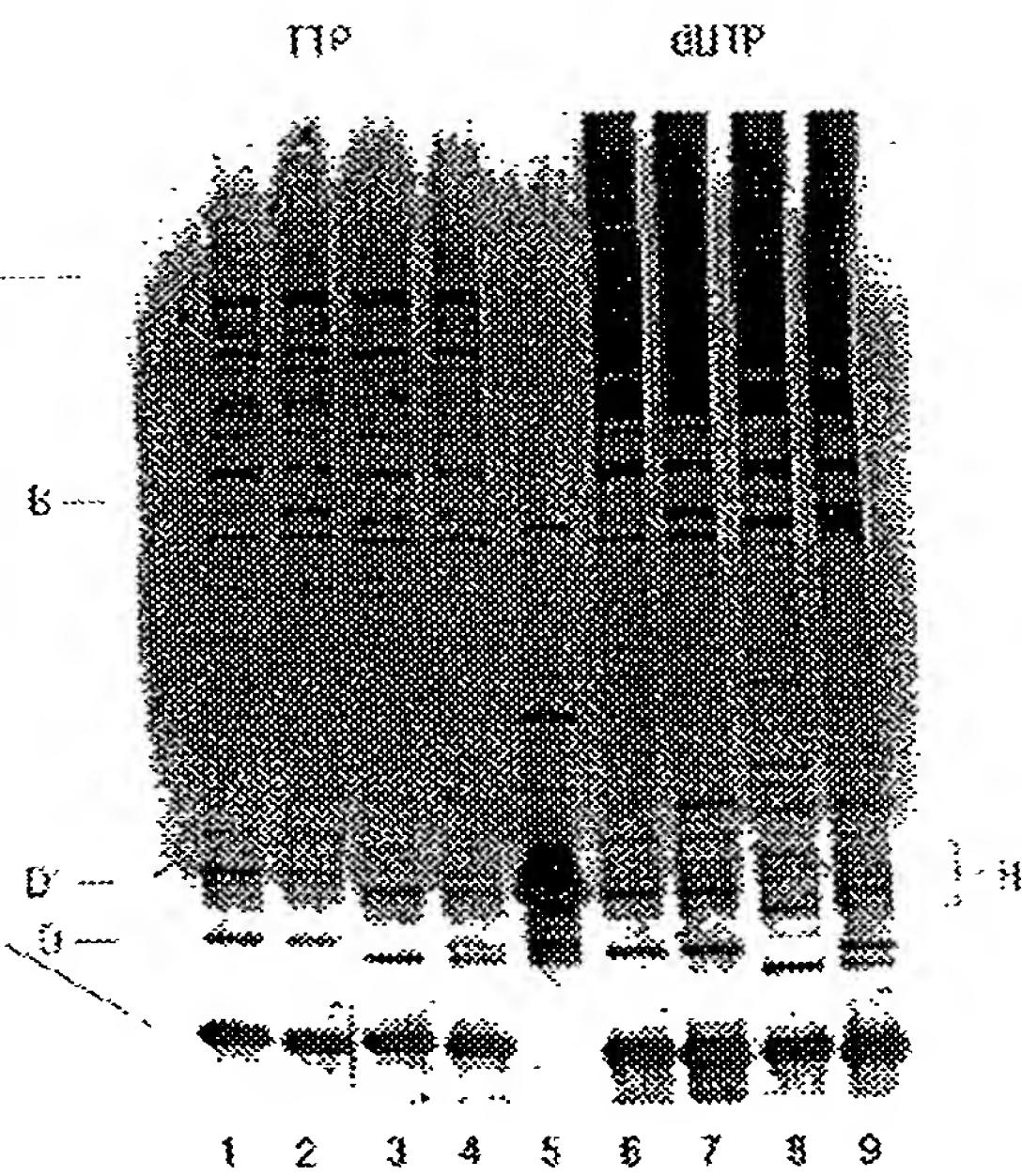
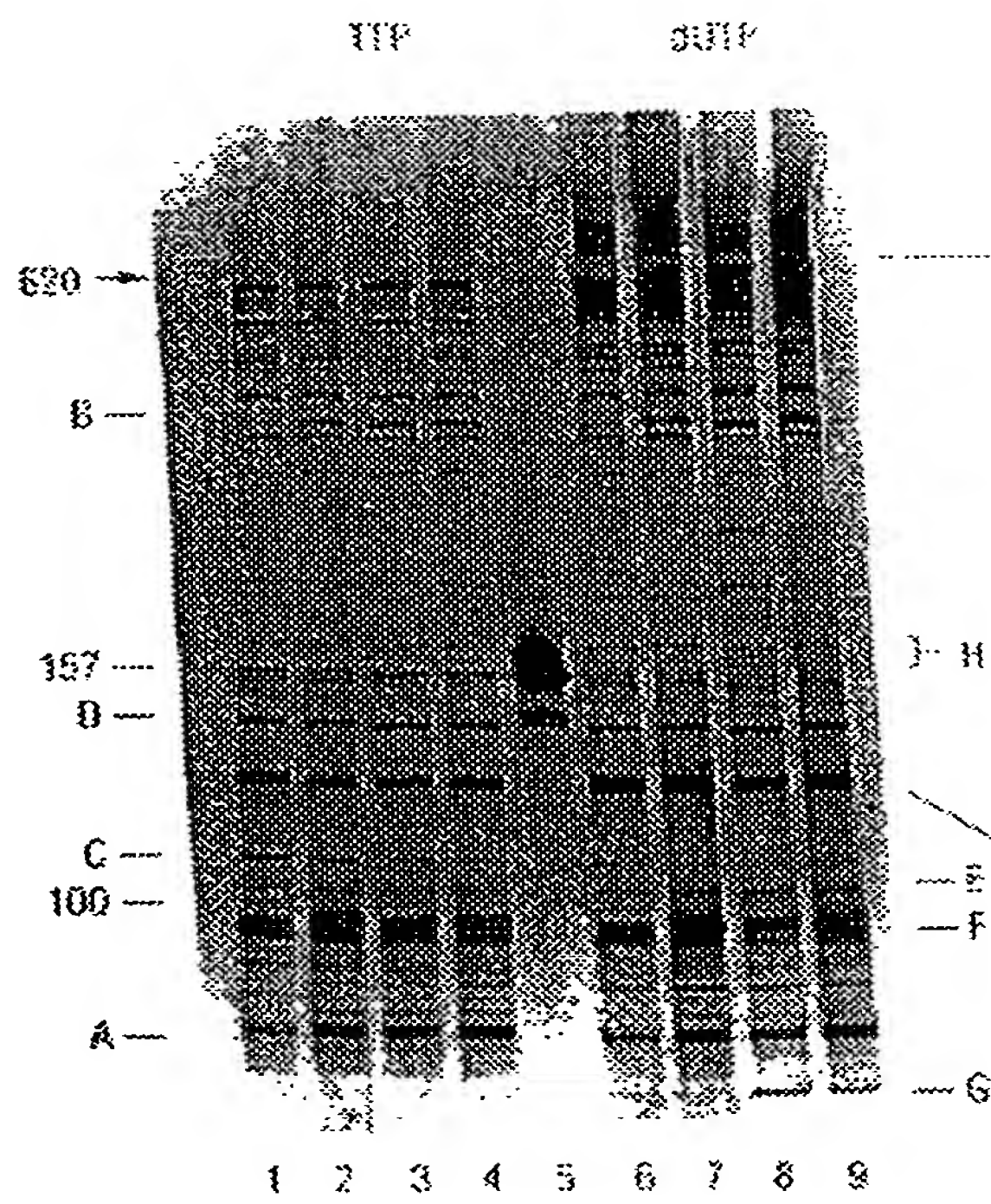


FIG. 84



U.S. PAT. OFF.

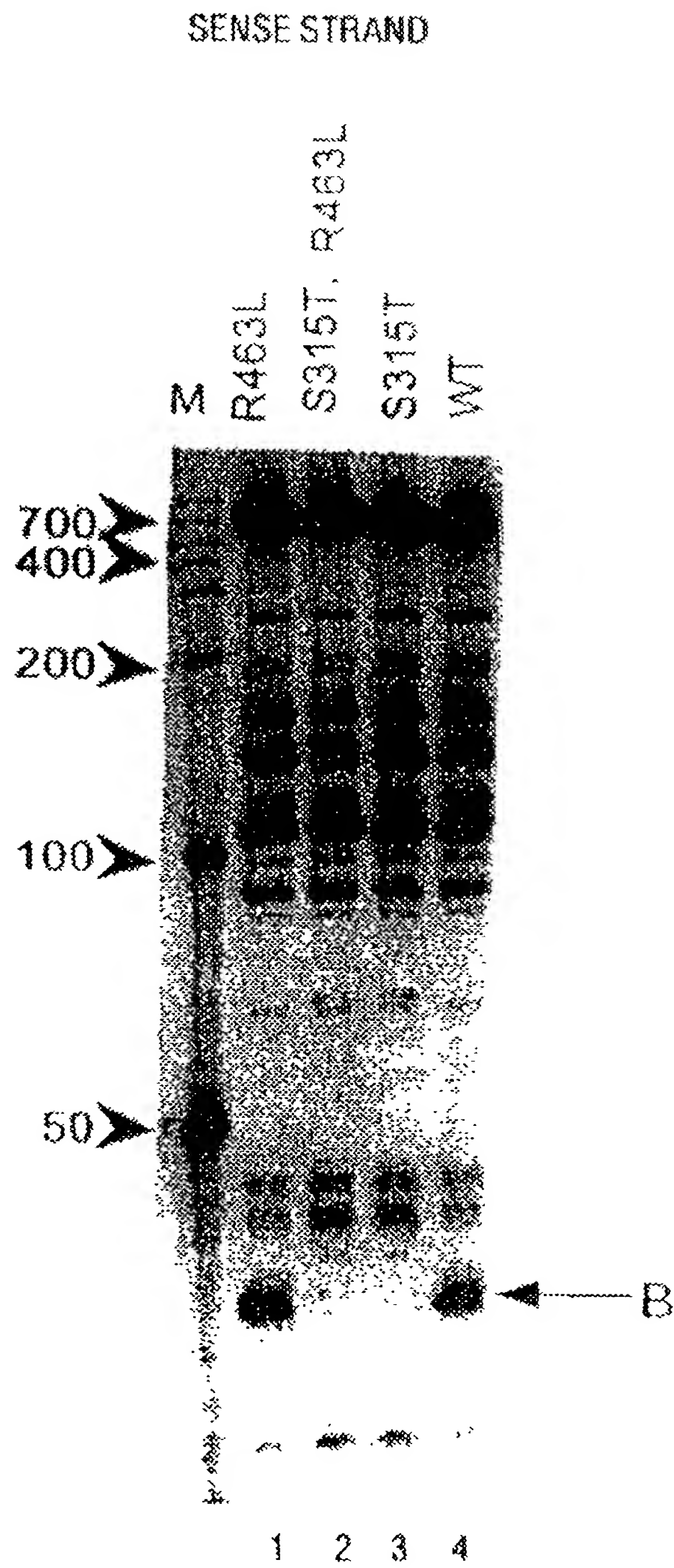


FIG. 86

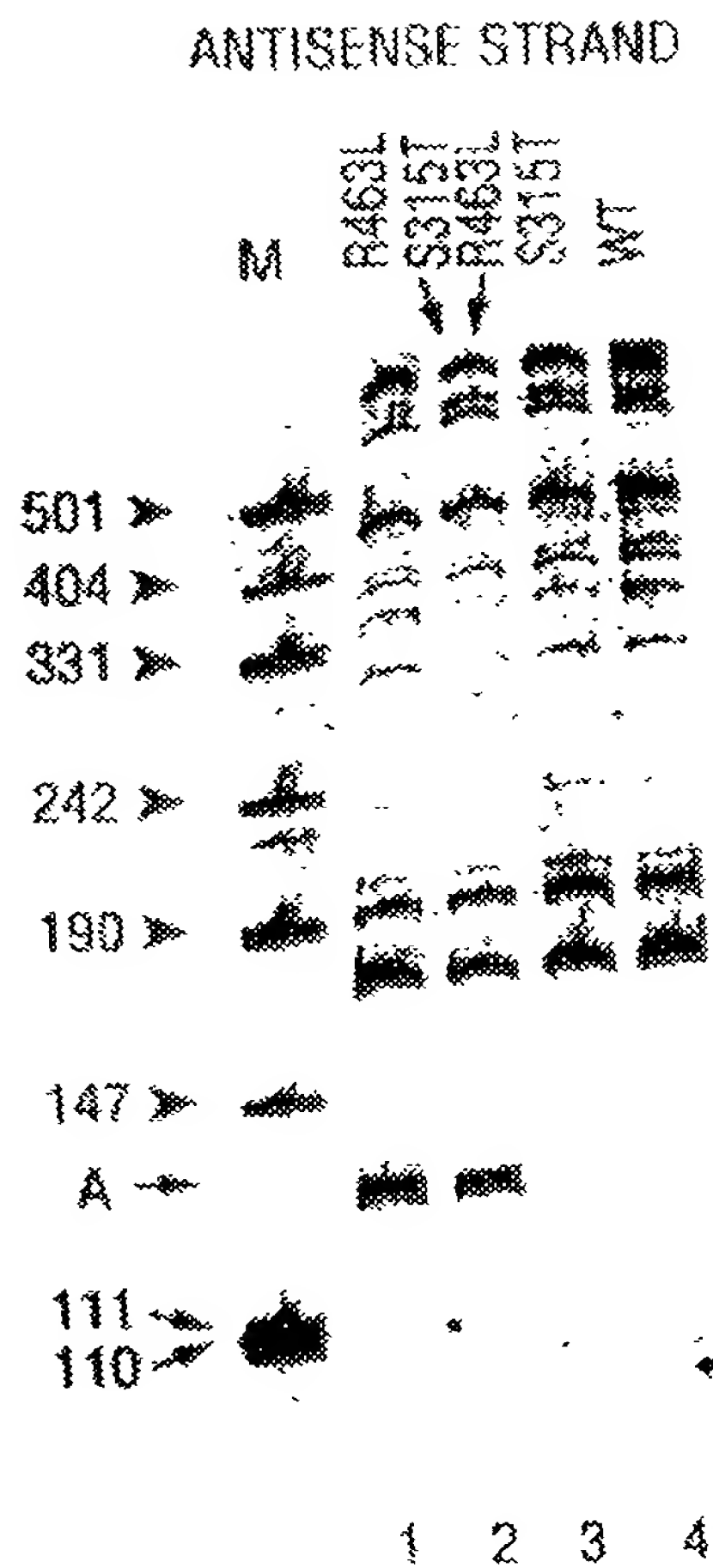


FIG. 87

10	20	30	40	50	60	1638
AGA	GTTTGATCCT	GGCTCAG				
AAATTGAAGA	<u>GTTTGATCAT</u>	<u>GGCTCAGATT</u>	GAACGCTGGC	GGCAGGCCTA	ACACATGCAA	
TTTAACTTCT	CAAACCTAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT	
70	80	90	100	110	120	ER10
				GGCGGAC	GGGTGAGTAA	
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	<u>AGTGGCGGAC</u>	<u>GGGTGAGTAA</u>	
CAGCTTGCCA	TTGTCCCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACATCATT	
130	140	150	160	170	180	
TGTCTGGGAA	ACTGCCCTGAT	GGAGGGGGAT	AACACTGGA	AACGGTAGCT	AATACCGCAT	
ACAGACCCCTT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGCAA	GACCAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCAGATG	
TTGCAGCGTT	CTGGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGTGGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA	
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT	
310	320	330	340	350	360	
GGATGACCCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG	
CCTACTGGTC	GGTGTGACCT	TGACTCTGTG	CCAGGTCTGA	<u>GGATGCCCTC</u>	<u>CGTCGTCACC</u>	
			TGA	GGATGCCCTC	CGTCGTC	1659

FIG. 88A

370 380 390 400 410 420
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT
CCTTATAACG TGTTACCCGC GTTCGGACTA CGTCGGTACG GCGCACATAC TTCCTCCGGA

430 440 450 460 470 480
TCGGGTTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATTT
AGCCCAACAT TTCATGAAAG TCGCCCCCTCC TTCCCTCATT TCAATTATGG AAACGAGTAA

490 500 510 520 530 540
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG
CTGCAATGGG CGTCTTCTTC GTGGCCGATT GAGGCACGGT CGTCGGCGCC ATTATGCCTC

550 560 570 580 590 600
GGTGCAAGCG TTAATCGGAA TTAAGCGCAC TAAAGCGCAC GCAGGCGGTT TGTTAAGTCA
CCACGTTTCG AATTAGCCTT ATGACCCCGC ATTTCCGGTG CGTCCGCCAA ACAATTTCAGT

610 620 630 640 650 660
GATGTGAAAT CCCC GGCGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC
CTACACTTTA GGGGCCCGAG TTGGACCCCTT GACGTAGACT ATGACCGTTC GAACTCAGAG

670 680 690 700 710 720
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTC GAGGAATACC
CATCTCCCCC CATCTTAAGG TCCACATCGC CACTTTACGC ATCTCTAGAC CTCCTTATGG

730 740 750 760 770 780
GGTGGCGAAG GCGGCCCCCTT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA
CCACCGCTTC CGCCGGGGGA CCTGCTTCTG ACTGCGAGTC CACGCTTTTCG CACCCCTCGT

FIG. 88B

790	800	810	820	830	840
AACAGGATTA	GATACCCTGG	TAGTCCACGC	CGTAAACGAT	GTCGACTTGG	AGGTTGTGCC
TTGTCCTAAT	CTATGGGACC	ATCAGGTGCG	GCATTTGCTA	CAGCTGAACC	TCCAACACGG
850	860	870	880	890	900
CTTGAGGCGT	GGCTTCCGGA	GCTAACGCGT	TAAGTCGACC	GCCTGGGGAG	TACGGCCGCA
GAACTCCGCA	CCGAAGGCCT	CGATTGCGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT
910	920	930	940	950	960
AGGTTAAAC	TCAAATGAAT	TGACGGGGGC	CCGCACAAGC	GGTGGAGCAT	GTGGTTTAAT
TCCAATTTTG	AGTTTACTTA	ACTGCCCCCG	GGCGTGTTCTG	CCACCTCGTA	CACCAAAATTA
970	980	990	1000	1010	1020
TCGATGCAAC	GCGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTTT	CAGAGATGAG
AGCTACGTTG	CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCTCTACTC
1030	1040	1050	1060	1070	1080
AATGTGCCCT	CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTCGTCAGCT	CGTGTGTGTA
TTACACGGAA	GCCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACAACACT
1090	1100	1110	1120	1130	1140
	GC	AACGAGCGCA	ACCC		
AATGTTGGGT	TAAGTCCCGC	AACGAGCGCA	ACCCTTATCC	TTTGTTGCCA	GCGGTCCGGC
TTACAACCCA	ATTCAGGGCG	TTGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCCG
1150	1160	1170	1180	1190	1200
				ATG	ACGTCAAGTC
				ATG	ACGTCAAGTC
CGGGAACTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC
GCCCCTTGAGT	TTCCCTCTGAC	GGTCACTATT	TGACCTCCTT	CCACCCCTAC	TGCAGTTTCAG

185

58-3
58-4

FIG. 88C

[illegible]

1210	1220	1230	1240	1250	1260	
ATCATGGCCC	TTA					SB-3
ATCATGGCCC	TTACGA					SB-4
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG	
TAGTACCGGG	AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC	
1270	1280	1290	1300	1310	1320	
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	
TGGAGCGCTC	TCGTTCCGCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG	
1330	1340	1350	1360	1370	1380	
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT	
AGCTGAGGTA	CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACIIATGCA</u>	1743
				GC	CACTTATGCA	
1390	1400	1410	1420	1430	1440	
TCCCCGGGCT	TGTACACACC	GCCCCGTCACA	CCATGGGAGT	GGGTTGCATA	AGAAGTAGGT	
AGGGCCCCGA	ACATGTGTGG	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCCTTCATCCA	
AGGGCCCCGA	ACATG					1743
1450	1460	1470	1480	1490	1500	
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	
TCGAAATTGA	AGCCCTCCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT	
1510	1520	1530	1540	1550		
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....		
GTTCCATTGG	CATCCCCCTTG	GACGCCCAACC	TAGTGGAGGA	AT.....		

FIG. 88D

09940925.022602

1638 (SEQ ID NO:151)	AGAGTTTGATCCTGGCTCAG
E.colirrsE (SEQ ID NO:158) 0	...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGGCTGGCGGCAGGCCTAACACATGCA
Cam.jejun5 (SEQ ID NO:159) 0	~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGGCTGGCGGCCTAATACATGCA
Stp.aureus (SEQ ID NO:160) 0	..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGGCTGGCGGCCTAATACATGCA
	GGCGGACGGG
ER10 (SEQ ID NO:152)	
E.colirrsE	60 AGTCGAACGGTAACAG----GAAGAAGCTTGCTTCTTT----GCTGACGAGTGCGGACGGG
Cam.jejun5	62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAGTGGA-----TTAGTGGCGCACGGG
Stp.aureus	61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG-----TT-AGCGGCGGACGGG
ER10	TGAGTAA
E.colirrsE	114 TGAGTAAATGTCTGGGA-AACTGCCCTGATGGAGGGGATAACTACTGGAACGGTAGCTAATA
Cam.jejun5	114 TGAGTAAAGGTATAGTTAACTCTGCCCTACACAAGAGGACAAACAGTTGGAACGACTGCTAATA
Stp.aureus	113 TGAGTAAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAACCGGAGCTAATA
E.colirrsE	175 CCGCATAAC-----GTGCGCAAGAC-----CAAAGAGGGGACCTTCG-GGCCCTCTTG
Cam.jejun5	176 CTCTATACTCCTGCTGCTTAACACACAAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
Stp.aureus	175 CCGGATAATAATTTTGAACCGCATGTTCAAAAGTGAAAGACGGT-----CTT-----GCTGTCA
E.colirrsE	221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTGGGTAAACGGCTCACCTAGGCGACGA
Cam.jejun5	221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
Stp.aureus	229 CTTATAGATGGATCCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA
E.colirrsE	283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACCTGAGACACGGTCCAGACTCCTA
Cam.jejun5	283 CGCTTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACCTGAGACACGGTCCAGACTCCTA
Stp.aureus	291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACCTGAGACACGGTCCAGACTCCTA
1659 (COMPL)	ACTCCTA

FIG. 89A

05940925.022602

E.colirrsE
Cam.jejun5
Stp.aureus
1659(COMPL)

E.colirrsE
Cam.jejun5
Stp.aureus

E.colirrsE
Cam.jejun5
Stp.aureus

345 C G G G A G G C A G C A G T G G G G A A T A T T G C A C A A T G G G C G C A A G C C T G A T G C A G C C A T G C C G C G T G
345 C G G G A G G C A G C A G T A G G G A A T A T T G C G C A A T G G G G A A C C C T G A C G C A G C A A C G C C G C G T G
353 C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A T G G G C G A A G C C T G A C G G A G C A A C G C C G C G T G
CGGGAGGCAGCAG

407 T A T G A A G A A G G C C T T C G G G T T G T A A A G T A C T T T C A G C G G G G A G G A A - G G G A G T A A A G T T A A T
407 G A G G A T G A C A C T T T T C G G A G C G T A A A C T C C T T T T C T T A G G G A A G - - - - - A A T T
415 A G T G A T G A A G G T C T T C G G A T C G T A A A C T C T G T T A T T A G G G A A G A A C A T A T G T G T A A G T A A C

468 A C C T T T G C T C A T T G A C G T T A C C C G C A G A A G C A C C G G C T A A C T C C G T G C C A G C A G C C G C G
455 C - - - - - T G A C G G T A C C T A A G G A A T A A G C A C C G G C T A A C T C C G T G C C A G C A G C C G C G
476 - T G T G C A C A T C T T G A C G G T A C C T A A T C A G A A G C C A C G G C T A A C T A C G T G C C A G C A G C C G C G

FIG. 89B

E.colirrse	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAGCGCACGCAGCGGGT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAGGGCGCGTAGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAGCGCGCGTAGCGGGTTT
E.colirrse	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGGAAACTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAAGCCCCACGGCTCAACCGTGGAGGTCATTGGAAACTGGAAACTT
E.colirrse	654	GAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAAATTGGTGGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp-aureus	662	GAGTGCAGAAAGAGGAAAGTGGAATTCCATGTGTAGCCGTGAAATGCGCAGAGATATGGAGGA
E.colirrse	716	ATACCGGTGGCGAAGGGGGCCCCCTGGACGAAGACTGACGCTCAGGTGCCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCGAAGGCGATCTGCTGGAACTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp.aureus	724	ACACCAGTGGCGAAGGCGACTTTCTGCTCTGTAACCTGACGCTGATGTGCCGAAAGCGTGGGGA
E.colirrse	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C

E.colirrsE	840	C=CTTGA=GGCGTGGCTTCCGGAGCTAACGGGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
Cam.jejun5	816	G=CTAGT-CATCTCAGTAATGCAGCTAACGCATTAAAGTGTAACCGCCTGGGGAGTACGGTCGC
Stp.aureus	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACGCATTAAAGCACTCCGCCTGGGGAGTACGACCCGC
E.colirrsE	900	AAGGTTAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
Cam.jejun5	876	AAGATTAAACTCAAAGGAATAGACGGGGACCCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
Stp.aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGACCCCGCACAAAGCGGTGGAGCATGTGGTTTAATT
E.colirrsE	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTTCAGAGATGAGAAT
Cam.jejun5	938	CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCTTTTAGAGATAAGAGG
Stp.aureus	971	CGAAGCAACGCGAAGAACCTTACCAATCTTTGACATCCTTTGACAACTCTAGAGATAGAGCC
E.colirrsE	1024	GTG=-CCTTCGGG=-AA=CCGTGAGACAGGTGCTGCATGGCTGTCTCAGCTCGTGTGTGA
Cam.jejun5	1000	GTGCTAGCTTGCTAGAA=CTTAGAGACAGGTGCTGCACGGCTGTCTCAGCTCGTGTGTGA
Stp.aureus	1033	TTCC=CCTTCGGG=-GGACAAAGTGACAGGTGCTGCATGGTTGTCTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
E.colirrsE	1081	AATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG=CC
Cam.jejun5	1061	GATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCACGTATTTAGTTGCTAACGGTTCGG=CC
Stp.aureus	1092	GATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA=TTAAGT=T

FIG. 89D

SB-3	(SEQ ID NO: 157)		ATGACGTCAAGTCATC
SB-4	(SEQ ID NO: 154)		ATGACGTCAAGTCATC
E.colirrsE	1142	GGGA	ACTCAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATC
Cam.jejun5	1122	GAGCA	CTCTAAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus	1152	GGGCA	CTCTAAGTTGACTGCCCGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATC
SB-3		ATGG	CCCCCTTA
SB-4		ATGG	CCCCCTTACGA
E.colirrsE	1204	ATGG	CCCCCTTACGACCAAGGGCTACACACGTGCTACAATGGCGCATACAAGAGAAGCGACCTC
Cam.jejun5	1183	ATGG	CCCCCTTATGCCCAAGGGCGACACACGTGCTACAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214	ATGG	CCCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAATACAAGGGCAGCGAAACC
E.colirrsE	1266	GCGA	GAGCAAGCGGACCTCATAAAGTGCGTCTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5	1245	GCGA	GGTGGAG-CAAACTCTATAAAATATGTCCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GCGA	GGTCAAGCAATCCCATAAAGTTGTTCTCAGTTCGGATTGTTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGA	AGTCGGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejun5	1306	CATGA	AGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus	1338	CATGA	AGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743(compl)			CGGTGAATACGTTCCCGGGC

FIG. 89E

<i>E. coli</i> rrSE	1389	CTTGTAACACCGCCCGTCACACCATGGGAGTGGGTGCAAAAGAAGTAGGTAGCTTAACCT
<i>Cam. jejuni</i> S	1368	CTTGTAACACCGCCCGTCACACCATGGGAGTTGATTTCACTCGAAGCCGGAATACT--A-A
<i>Stp. aureus</i>	1399	ATTGTACACACCGCCCGTCACACCAACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCT
1743(compl)		CTTGGTAC
<i>E. coli</i> rrSE	1451	TCG-GGAGGGCGCTTACCACCTTTGTGATTCATGACTGGGGTGAGTCGTAAACAAGGTAACCG
<i>Cam. jejuni</i> S	1427	AC--T-AGTTACCGTCCACAGTGGAATCAGCGACTGGGGTGAGTCGTAAACAAGGTAACCG
<i>Stp. aureus</i>	1461	TTTAGGAGCTAGCCGTGGAAGGTGGGACAAATGATTGGGGTGAGTCGTAAACAAGGTAACCG
<i>E. coli</i> rrSE	1512	TAGGGGAACCTGCGGTTGGATCACCTCCTTA---
<i>Cam. jejuni</i> S	1485	TAGGAGAACCTGCGGTTGGATCACCTCCT-----
<i>Stp. aureus</i>	1523	TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-

[illegible]

FIG. 89F

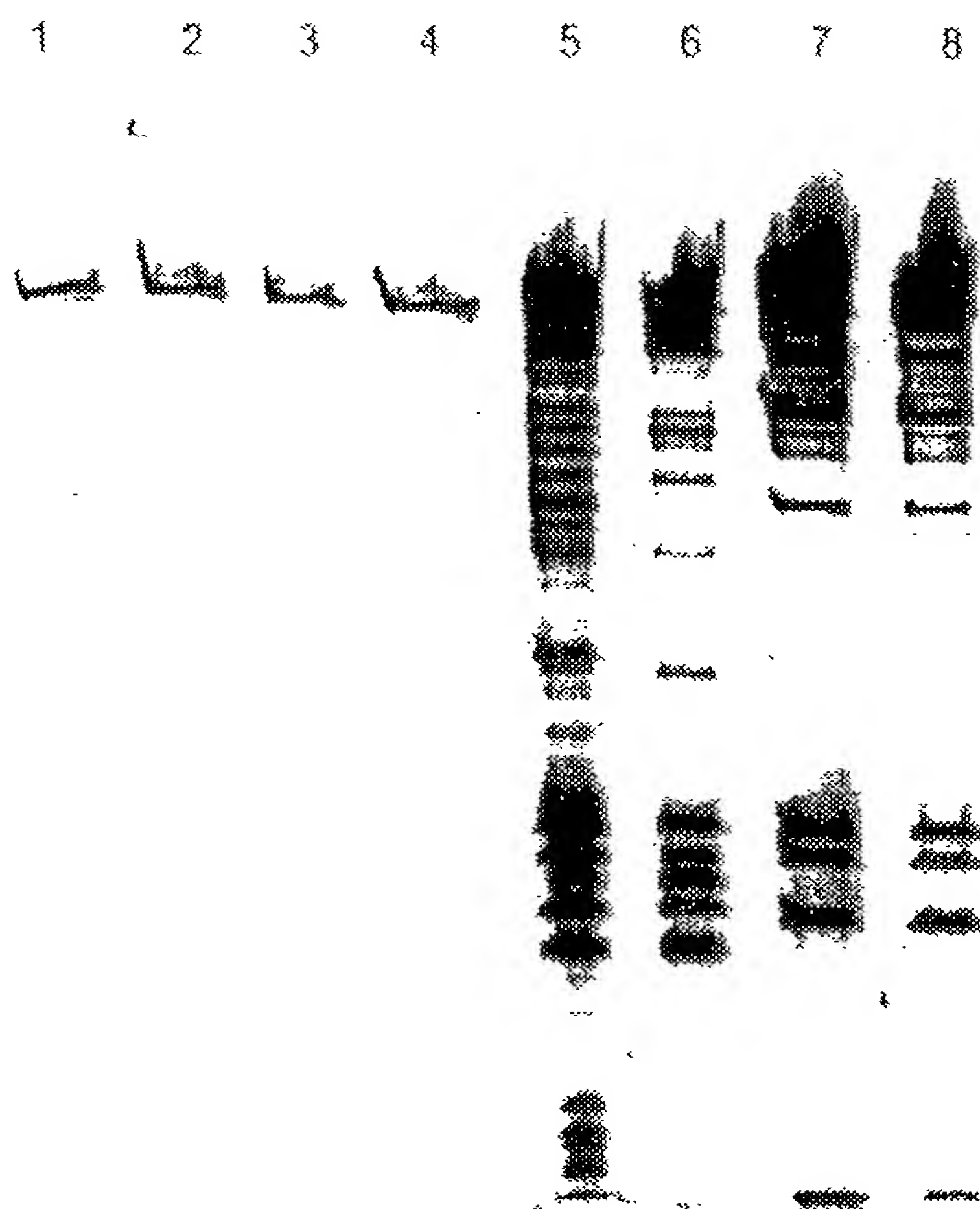


FIG. 90



Figure 1 is a black and white photograph of a gel electrophoresis result. The gel has 10 lanes, numbered 1 to 10 at the top. Lane 1 shows a single, dark, high-molecular-weight band. Lanes 2 through 5 show a series of bands at lower molecular weights, indicating degradation of the polymer. Lanes 6 through 10 show a similar pattern of bands, but with varying intensities and positions, suggesting different degradation rates or products. To the right of the gel, there are several horizontal lines representing molecular weight markers, with some numbers (100, 200, 300, 400, 500, 600, 700, 800, 900, 1000) visible next to them.

FIG. 91B

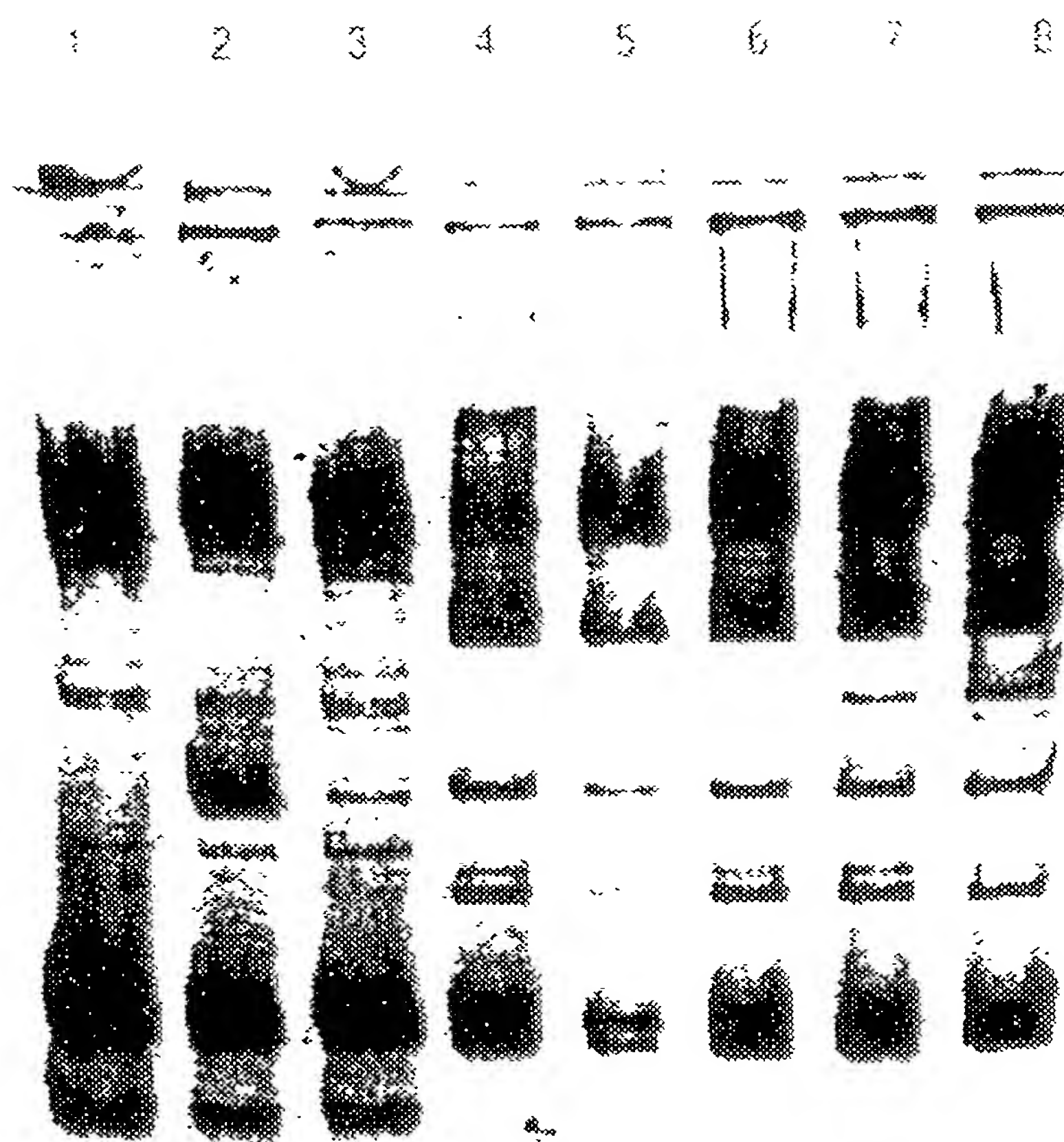


FIG. 93



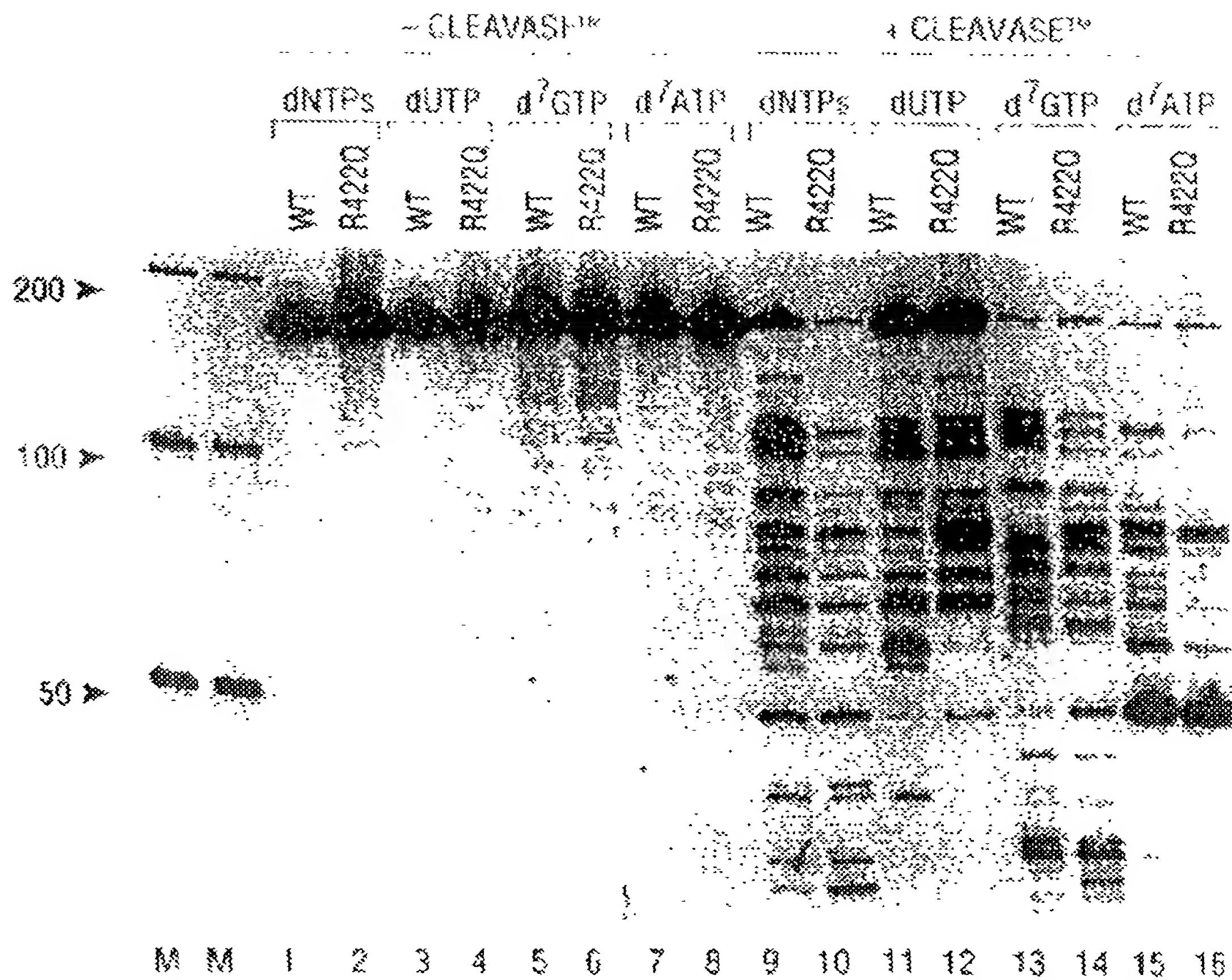


FIG. 94